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AAU27697
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Human PRO1106 (UNQ
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Skin cell protein,
Novel human diagno
Human ORFX ORF2093
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| 369 | 380.5 | 382.5 | • | 412 | 417 | 432.5 | 432.5 | 445 | 446 | 446 | 446 | 446 | 454.5 | 454.5 | 454.5 | 455.5 | 479 | 505.5 | 508 | 508 | 508 | 521 | 632 | 761 | 800.5 | 841 | 902 | 910 | 910 | 1037 | 1143 | 1143 | 1241 |
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| Human polypeptide | | Arabidopsis thalia | Drosophila melanog | Arabidopsis thalia | Arabidopsis thalia | | Arabidopsis thalia | Arabidopsis thalia | | Arabidopsis thalia | | | | thal | \mathbf{r} | | Novel human diagno | 0 | Arabidopsis thalia | | Arabidopsis thalia | Arabidopsis thalia | Human uncoupling p | Human polypeptide, | Human polypeptide | Human protein SEQ | Drosophila melanog | = | | ם | Novel human calciu | polypeptic | Human membrane tra |

ALIGNMENTS

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RESULT
AAM79077
03-FEB-2000;
27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
                                                                                                                                                                                                 Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; humnomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                         09-AUG-2001.
                                                                                                                                                                                                                                                  Human protein SEQ ID NO 1739.
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2000US-0560875.
2000US-0598075.
2000US-0620325.
2000US-0654936.
2000US-0633561.
2000US-0693325.
2000US-0728422.
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Matches 475;
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                                       dlavyellksywldnfakdsvnpgvmvllgcgalsstcgqlasyplalvrtrmqaqamle
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, Zhang J, Ren F, C
n T, Goodrich R;
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RESULT
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AAU27697

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Query Match Best Local

Similarity

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Score Pred.

1552.5; DB 2 No. 2.3e-133;

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Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat; mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia; cancer; lymphoma; neuroblastoma; autoinmune disorder; cell proliferation; nervous system disorder; inflammatory disorder; cell differentiation; angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn; genetic disorder; bone regeneration; tendon; ligament; tissue repair; cytostatic; antirheumatic; antiarthritic; vulnerary; antiinflammatory; antibacterial; immunosuppressive; vasotropic; antiparkinsonian; neuroprotective; osteopathic; antidiabetic; antiasthmatic; antiallergic; immunostimulant; analgesic; gene therapy.
                                                    disorders such as Parkinson's disease, Alzheimer's disease, Huntington's chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and Wernicke disease, inflammatory disorders such as nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis and inflammatory bowel disease. The sequences exhibit activity relating to angiogenesis, cell proliferation, cell differentiation, stem cell growth factor, activin or inhibin. Therefore, they can be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, accidental damage or genetic disorders. The sequences may also be used for regeneration of bone, cartilage, tendons and ligaments and in tissue repair and burn healing. Note: Some sequences for this patent did not form part of the printed specification, but were obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                  various types of disorder in a mammalian subject such as a human, dog, monkey, mouse, hamster or rat. The disorders include cancers such as leukaemia, lymphoma and neuroblastoma, autoimmune disorders such as multiple sclerosis, connective tissue disease, rheumatoid arthritis, diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system
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Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                               Sequences AAU27676-AAU28019 represent full-length polypeptides and contig polypeptides of the invention. The proteins and their associated DNA sequences are useful for the treatment, diagnosis and prevention of various types of disorder in a mammalian subject such as a human, dog,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis, treatment of cancer, neurological, inflammatory disorders and for use in array
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18-MAY-2000; 2000US-0577409;

17-JUN-2000; 2000US-0597707,

14-JUL-2000; 2000US-0616807.

19-SEP-2000; 2000US-0664641.
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18-MAY-2000;
17-JUN-2000;
14-JUL-2000;
19-SEP-2000;
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                                                                                                                                                                                                                                                                                07-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
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2000US-0577409.
2000US-0597707.
2000US-0616807.
2000US-0664641.
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Query Match Best Local Matches

Similarity

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Conservative

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multiple sclerosis, connective tissue disease, rheumatoid arthritis, disbetes mellitus, allergic rhinitis, asthma and eczema, nervous system disorders such as Parkinson's disease, Alzheimer's disease, Huntington's chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and Wernicke disease, inflammatory disorders such as nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis and inflammatory bowel disease. The sequences exhibit activity relating to angiogenesis, cell proliferation, cell differentiation, stem cell growth factor, activin or inhibin. Therefore, they can be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, accidental damage or genetic disorders. The sequences may also be used for regeneration of bone, cartilage, tendons and ligaments and in tissue repair and burn healing.
                                                                                                                                                                                                                                                                                                                                                                                  DNA sequences are useful for the treatment, diagnosis and prevention various types of disorder in a mammalian subject such as a human, dog monkey, mouse, hamster or rat. The disorders include cancers such as leukaemia, lymphoma and neuroblastoma, autoimmune disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT,
Xue AJ,
                                                        cartilage, tendons and ligaments and in tissue repair and burn healing. Note: Some sequences for this patent did not form part of the printed specification, but were obtained in electronic format directly from WIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequences AAU27676-AAU28019 represent full-length polypeptides and contig polypeptides of the invention. The proteins and their associated DNA sequences are useful for the treatment, diagnosis and prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
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                                      ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Page 126-127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptides and nucleic acids obtained from cDNA libraries red from various human tissues, for diagnosis, treatment of r_{\ell} neurological, inflammatory disorders and for use in arrays
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T, Wang J,
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Ma Y, Wang
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ang D, Chen
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253 222 162 133 282 193 102 73 45 DAEQPTRYETLFQALDRNGDGVVDIGELQEGLRNLGIPLGQD----AEEXIFTTGDVNKD GNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIYPMEVM GKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQAELILQ 132 gnginvlkiapesaikfmayeqikrailgqqetlhvqerfvagslagataqtiiypmevl mwwkqlvagavagavsrtgtapldrlkvfmqvhasktnrlnilgglrsmvleggirslwr QWWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQMVKEGGIRSLWR |:| |||||:|| ||||:|| : ::|::: |||||| :||: ||:|||:: || :|| smdrdgtmtidwqewrdhfllhslenvedvlyfwkhstvldigecltvpdefskqekltg SIDVDGTMTVDWNEWRDYFLFNPVTDIEEIIRFWKHSTGIDIGDSLTIPDEFTEDEKKSG daerrqrwgrlfeeldsnkdgrvdvhelrqglarlg--85; Score 1552.5; Pred. No. 2.6e 35; Mismatches ggnpdpgaqqgissegdadpd Indels 7; Gaps 341 221 192 101 161 2

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RIISKEGIPGLYRGITPNFMKVLPAVGISYVVYENMKQTLGVTQK

KTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYELLKSYW

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; receptor immunoadhesin; gene mapping.
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                                                                                                                                                                                                                                                                                                                                                                                                                sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recemblant techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polynucleotides encoding them. The PRO sequences of the invention we identified based on extracellular domain homology screening. The PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention provides membrane-bound PRO polypeptides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        claim
                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Membrane-bound proteins and related nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                        recombinant techniques.
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                                                                                                                OMVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAG
                                                                                                                                                       ATAQTFIYPMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAG
                                                                                                    {\tt qmireggarslwrgnginvlkiapesaikfmayeqikrlvgsdqetlriherlvagslag}
                                                                                                                                                                                                                                                           IDLAVYELLKSYWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAML
                                                  aiaqssiypmevlktrmalrktgqysgmldcarrilaregvaafykgyvpnmlgiipyag
                                                                                                                                                                                  IPDEFTEDEKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFR
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12; Fig 206; 822pp; English.
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Yuan J;
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98US-0098024
98US-0116545
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                                                                                                                                                                                                                                                                                                             Score 1501; DB 21;
Pred. No. 1.2e-128;
1; Mismatches 72;
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01-MAR-2000

03-MAR-2000

25-MAY-2000

25-MAY-2000

25-MAY-2000
                  The present sequence is a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as molecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping.
                                                                                                                                                                                                                     Eaton DL,
Grimaldi (
                                                                                                                                            Eighty four nucleic acids encoding PRO polypeptides, useful in molecular biology, including use as hybridization probes, and chromosome and gene mapping.
Sequence
                                                                                                                   Claim 12; Fig 58; 278pp; English.
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DB; AAF92086.
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99US-0170262.
2000US-0175481.
2000WO-US04341.
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AL,
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Watanabe
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24-FEB-2000

02-MAR-2000

15-MAR-2000
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26-JUL-1999;
28-JUL-1999;
17-AUG-1999;
15-SEP-1999;
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08-OCT-1999;
30-NOV-1999;
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16-DEC-1999;
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07-JUL-1999;
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cell death;
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99US-0145698

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99US-014522

99US-01531096

99WC-US21547

99WC-US2163

99WC-US28313

99WC-US28314

2000WC-US2814

2000WC-US03565

2000WC-US04914

2000WC-US04814

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l mapping; ge
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Ferrara N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bloactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12;
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                                                                                                                                                                                                                                                                                                                                        EEKIFTTGDVNKDGKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLG 119 ::|| || :||:||:||:|| || ||:||:|| || kgkivqagdkdldgqldfeefvhylqdhekklrlvfkildkndgrldaqeimqslrdlg 111
                                                                                                                                                           QMVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAG
                                                                                                  \verb|aiaqssiypmevlktrmalrktgqysgmldcarrilaregvaafykgyvpnmlgiipyag|
                                                                                                                                                                                                                                       ATAQTFIYPMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGTIPYAG
                                                                                                                                                                                                                                                                                                                                                                                                    vkiseqqaekilksmdkngtmtidwnewrdyhllhpvenipeiilywkhstifdvgenlt
                                                                                                                                                                                                                                                                                                                                                                                                                  LTISEQQAELILQSIDVDGTMTVDWNEWRDYFLFNPVTDIEEIIRFWKHSTGIDIGDSLT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-032160/04.
DB; AAF44204.
                                                                                                                              EGSPQLNMVGLERRIISKEGIPGLYRGITPNEMKVLPAVGISYVVYENMKQTLGVTQK
                                                                                                                                                                                                                                                                                  qmireggarslwrgnginvlkiapesaikfmayeqikrlvgsdqetlriherlvagslag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 zi AJ, Baker KP, Botstein D, Desnoyers L, Eaton
N, Fong S, Gerber H, Gerritsen ME, Goddard A,
i CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J,
Stewart TA, Tumas D, Watanabe CK, Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fig 206; 935pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to produce polypeptides used to target
as toxins, radiolabels or antibodies,
targeted cell death -
                                                                                                                                                                                                                                     71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1501; DB 22;
Pred. No. 1.2e-128;
1; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eaton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      469;
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PRO nucleotide
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Wood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                       469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WI;
                                                                                                                                                                                                                                                                                                                                                                          239
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                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                    cells. Polypeptides of the invention may be used to stimulate cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle disorders. Sequences AAY75942-Y76123 represent polypeptides encoded by CDNA sequences AAY75942-Y7617, AAY76020-Y76021, AAY76094-Y76104 and types. Sequences AAY75942-Y75947, AAY76020-Y76021, AAY76094-Y76104 and types.
                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                        AAY76119 are proteins with an N-terminal signal sequence, indicating that they are secreted. Sequences AAY75986-Y75989, AAY76061-Y76071, AAY76106-Y76109 and AAY76121-Y76122 are proteins with one or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
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09-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09955865-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anti-inflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            secreted;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine
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   240
                                172
                                                            180
                                                                                         112
                                                                                                                   120
                                                                                                                                                 52
                                                                                                                                                                              60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to novel nucleic acid sequences derived from rat mal papilla, human keratinocytes and neonatal foreskin fibroblasts, mouse embryonic skin, keratinocyte stem cells and transit amplifying 1s. Polypeptides of the invention may be used to treat inflammation,
                                                                                                                                           \verb|kqkivqagdkdldgqldfeefvhylqdhekklrlvfksldkkndgridageim| qslrdlg|
                                                                                                                                                             EEKIFTTGDVNKDGKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLG
QMVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAG
                           vpdeftveerqtg \verb|mwwrhlvagggagavsrtctapldrlkvlmqvhasrsnnmcivggft|
                                            IPDEFTEDEKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFR
                                                                                     vkiseqqaekilksmdkngtmtidwnewrdyhllhpvenipeiilywkhstifdvgenlt
                                                                                                                  LTISEQQAELILQSIDVDGTMTVDWNEWRDYFLFNPVTDIEEIIRFWKHSTGIDIGDSLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dermal papilla; keratinocyte; neonatal for onic skin cell; keratinocyte stem cell; to ted; transmembrane; inflammation; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polynucleotides useful for the ling wounds and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Page 199-200; 235pp;
                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ۲
                                                                                                                                                                                                                                                                                    469 AA;
                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorder; skin wound; hair follicle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumour vascularisation; growth disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0069726.
98US-0188930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-NZ00051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatic; neuroprotective; vulnery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  & DEV CORP
                                                                                                                                                                                                                      60.4%;
65.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ĭ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Watson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  family protein,
                                                                                                                                                                                                                        Score 1499;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JD,
                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Onrust
                                                                                                                                                                                                                          .8e-1
                                                                                                                                                                                                                                      DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ
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                                                                                                                                                                                                                        21;
128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      foreskin fibroblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurological
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorder;
                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                      Length
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                                                                                                                                                                                                                                      469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murison
                                                                                                                                                                                                         0,
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell;
                                                                                                                                                                           119
                                                         239
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                                                                                                                                                                                                         0;
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Qy

60

EEKIFTTGDVNKDGKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLG 119

Query Match Best Local S Matches 274

l Similarity 274; Conser

Conservative

60.4%;

Score 1499; D Pred. No. 1.8e 73; Mismatches

DB 22; .8e-128; les 71;

Indels Length

0;

Gaps

0,

1499; No. 1

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AAB56023
ID AAB5
                                                        The present sequence is a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer c modulating angiogenesis, inhibiting angiogenesis and vascularisatio tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency (HIV)-1 to leukocytes, and treating inflammatory disease, cancer a neurological diseases. The polynucleotide can be used as a marker, the identification of genetic disorders, and for the design of
                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide used in the identification of genetic disorders and encoding polypeptides used for treating inflammatory disease, cancer and neurological diseases.
Sequence
                                                                                                                                                                                                                                                                                  Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Watson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENE-) GENESIS RES & DEV CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               keratinocyte growth stimulation; cancer; angiogenesis inhibition; inflammation; neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse; skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB56023;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               412 egapevtmsslfkqilrtegafglyrglapnfmkvipavsisyvvyenlkitlgvqsr 469
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)B; AAC99722, A
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                                                                                                                                                                                                                                                                                Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neuroprotective; vulnerary; immunomodulatory;
  469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strachan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell; cytostatic; antiinflammatory; anti-HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                              266-267; 352pp; English.
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                                        examining
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                                        expression
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                                        patterns.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kumble
                                                                                                                                                                      wth of cancer cells vascularisation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ξĎ,
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RESULT
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and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving
                                     The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation pr polymerase chain reaction (PCR) primers, oligomers, and for cand gene mapping, and in recombinant production of (II). The
                                                                                                                            diagnostics, forensics, responsible for genetic biodiversity
                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                             31-MAR-2000;
23-AUG-2000;
                                                                                                     Claim
                                                                                                                                                                                                                               Drmanac
                                                                                                                                                                                                                                                       (HYSE-)
                                                                                                                                                                                                                                                                                                                   30-MAR-2001;
                                                                                                                                                                                                                                                                                                                                            11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                   WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                   food
                                                                                                                                                                                                                                                                                                                                                                                                                                Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG22637;
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supplement; medical imaging; diagnostic; genetic c
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)B; AAS86824.
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                                                              olated polynucleotide (I) and(I) is useful as hybridisation probes,
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                                                   chromosome
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Best Local S
Matches 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acids sequences of the invention.
                               Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotectivanticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiarimmunostimulant; thrombolytic; coagulant; vasotropic; antidabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
                   antianaemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ggldleefsrylqereqrlllmfhsldrnqdghidvseiqqsfralgisilleqaeknfa 161
                                                                                                                                                                                                                                                                                                                                                           FRRIISKEGIPGLYRGITPNFMKVLPAVGISYVVYENMKQTLGVTQK
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277; Conserv
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                                                                                                                                                    ORF2093 polypeptide sequence
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gene therapy; cancer;
ative disorder; osteoa
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                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                       entry)
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Pred. No. 1.3e
85; Mismatches
                                                                                                                                                                                                                                                           A
                   proliferative disorder;
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                                                                                                     nootropic; neuroprotective;
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                                                                                                                                                                                                                                                                                                                                             508
                   hypertension;
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02-APR-1999;
05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proliferative disorders, neurodegenerative disorders, osteoarthriti graft vs host disease, cardiovascular disease, diabetes mellitus, hypothyroidism, cholesterol ester storage, systemic lerythematosus, severe combined immunodeficiency (SCID), AIDS, viral bacterial or fungal infection, malaria, autoimmune disorders, asthmallergies, aplastic anaemia, burns, wounds, bone and cartilage dama nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetto; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antivital; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                    LDRLKIMMQVHGSKSDKMNIFGGFRQMVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQ
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nucleic acids and peptides derived from open reading for treating e.g. cancers, proliferative disorders,
                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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99US-0127636.
99US-0127728.
2000US-0540763.
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                                                                                                                                                                                                                                                                                                                                                       63;
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Pred. No. 5.6e
63; Mismatches
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.6e-119;
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                       in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                 Tang
immunosuppressant and cytostatic activity. The polynucleotides are usefu in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as
                                                                                                                                                                                                    Novel nucleic such as centra
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19-OCT-2000;
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2000US-0552317.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transporter polypeptide; insonian; anticonvulsant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          366 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cardiant; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                       2000US-193549P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hepatotropic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antianginal;
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Pred. No. 1.1e-112;
51; Mismatches 62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy;
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cc assays, monitoring clinical trials, pharmacogenetics) and therapeutic act as modulating agents in regulating variety of cellular processes, e.g. cellular proliferation, growth, differentiation or migration, immune cc responses, hormonal responses, inter- or intra-cellular communication. Growth, differentiation or migration, immune cc responses, hormonal responses, inter- or intra-cellular communication. The MTP molecules provide novel diagnostic targets and therapeutic agents to control transporter-associated disorders, e.g. Alzheimer's disease, ca autonomic function disorders (e.g. hypertension and sleep disorders such as cognitive and neurodegenerative disorders, e.g. Alzheimer's disease, ca neuropsychiatric disorders (e.g. hypertension and sleep disorders), comemory disorders (e.g. amnesia or age-related memory loss), bipolar cc malcules are also useful for treating cardiac-related disorders (e.g. arterioscierosis), disorders of the musculoskeletal system such as comparalysis and muscle weakness, cellular proliferation, differentiation or growth disorders including cancer e.g. carcinoma, sarcoma or leukemia, tumor angiogenesis and metastasis, hepatic disorders and hematopoietic cand/or myeloproliferative disorders. The molecules are also useful for treating hormonal disorders, such as diabetes mellitus, pituitary condulate the import and export of molecules from cells, e.g. hormones, condulate the import and export of molecules from the cell or facilitate the compartmentalization of the molecules into a sequestered conficiency disorders. The molecules into a sequestered conficiency disorders. (e.g. the molecules from the cell or facilitate the compartmentalization of the molecules into a sequestered conficiency disorders. (e.g. the molecules into a sequestered conficiency disorders.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention provides a novel human membrane transporter polypeptide (MTP). The MTP polypeptide can be expressed by standard recombinant methodology. MTP polypeptides, polynucleotides and antibodies are useful in screening assays, predictive medicine (diagnostic assays, prognostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human membrane transporter polypeptides and polynucleotides diagnosis, prevention and treatment of central nervous system, ceproliferation, hormonal, immune and cardiac-related disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 13; Fig 1A-B; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proliferation,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in screening assays,
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PR: AAI66980, AAI66981.
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useful

Sequence 461

human MTP

(clone Fbh32449).

intracellular space (e.g. the peroxisome) and modulate transport biological molecules across membranes, e.g. the plasma membrane membrane of the mitochondrion, peroxisome, lysosome, endoplasmic reticulum, nucleus or the vicuole. The present sequence represent

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                                                                                                                                                                         GKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQAELILQ 132
                                                                                                                                                                                                                                  DAEQPTRYETLFQALDRNGDGVVDIGELQEGLRNLGIPLGQD----AEEKIFTTGDVNKD
gnginvlkiapesaikfmayeqikrailgqqetlhvqerflagslagataqtiiypmevl
            GNGTNVIKIAPETAVKEWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIYPMEVM
                                                                  QWWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQMVKEGGIRSLWR
                                                                                                         daerrqrwgrlfeeldsnkdgrvdvhelrqglarlg---ggnpdpgaqqgissegdadpd
                                                      mwwkqlvagavagavsrtgtapldrlkvfmqvhasktnrlnifgglrsmvleggirslwr
                                                                                                                                     SIDVDGTMTVDWNEWRDYFLFNPVTDIEEIIRFWKHSTGIDIGDSLTIPDEFTEDEKKSG
                                                                                                                                                                                                                                                                          Conservative
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Pred. No. 7.6e-105;
78; Mismatches 87;
                                                                                                                                                                                                                                                                                                     Length
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RESULT 1
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    18-APR-2000;
119-MAY-2000;
07-JUN-2000;
07-JUL-2000;
07-JUL-2000;
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11-JUL-2000;
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11-JUL-2000;
11-JUL-2000;
11-AUG-2000;
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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7-MAR-2000;
3-APR-2000;
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  2000US-0179065.
2000US-0184664.
2000US-0184664.
2000US-0189874.
2000US-0199123.
2000US-0294515.
2000US-0216486.
2000US-0216486.
2000US-0216687.
2000US-0216880.
2000US-0217487.
2000US-0217487.
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2000US-0217487.
2000US-0217487.
2000US-0225214.
2000US-0225214.
2000US-0225276.
2000US-0225277.
2000US-0225277.
2000US-0225277.
2000US-0225778.
2000US-0225778.
2000US-02266681.
2000US-02266681.
2000US-0228277.009.
2000US-0228277.009.
2000US-0228277.09.
2000US-0228277.09.
2000US-0228287.
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21-SEP-2000
21-SEP-2000
25-SEP-2000
25-SEP-2000
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2000US-0231968

2000US-023399

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2000US-0233063

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17-NOV-2000; 17-NOV-2000;

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                                                                                                                                                                                   The invention relates to human polynucleotides (AAI63803-AAI64012) and CC the encoded proteins (AAM43497-AAM43660) useful for preventing, treating CC or ameliorating medical conditions e.g. by protein or gene therapy. The CC genes were isolated from a range of human tissues disclosed in the CC specification. The nucleic acids, proteins, antibodies and (ant)agonists CC are useful in the diagnosis, treatment and prevention of: (a) cancer, CC e.g. breast and ovarian cancer and other cancers of the adrenal gland, CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or CC urogenital; (b) immune disorders e.g. Addison's disease, allergies, CC autoimmune hamolytic anaemia, autoimmune thyroiditis, diabetes mellitus, CC crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative CC clitis; (c) cardiovascular disorders such as myocardial ischaemias; CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal CC and parasitic infections.

CC Note: The sequence data for this patent did not form part of the CC printed specification, but was obtained in electronic format directly cxx
                                                                                                              Query Match
Best Local s
Matches 219
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05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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05-DEC-2000;
                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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N-PSDB; AAI63830.
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 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isolated nucleic
                                                    ekifttgdvnkdgkldfeefmkylkdhekkmklafksldknndgkieaseivqslqtlgl
                          EKIFTTGDVNKDGKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGL 120
                                                                                                              al Similarity
219; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and/or preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ
                                                                                                                                                                                   244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barash SC,
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2000US-0249214.
2000US-0249215.
2000US-0249217.
2000US-0249217.
2000US-0249244.
2000US-0249245.
2000US-0249245.
2000US-0249265.
2000US-0249297.
2000US-0249300.
2000US-0250160.
2000US-0251030.
2000US-0251030.
2000US-02511988.
2000US-02511856.
2000US-02511868.
2000US-02511868.
2000US-0251869.
                                                                                                              Conservative
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                                                                                                                          46.18;
94.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruben
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human diseases and disorders
                                                                                                            Score 1143; Di
Pred. No. 2.7e
0; Mismatches
                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptides, useful for
                                                                                                                           .7e-96;
                                                                                                                                           DB
                                                                                                              12;
                                                                                                                                          22;
                                                                                                                                        Length
                                                                                                            Indels
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                                                                                                            0;
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                                                      73
                                                                                  60
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RESULT 1
ID 19941
ID 10941
ID 10941
XX AAU1
XX Huma KW Linmu KW Linmu WO2(
XXX Homc XX Homc XX Home XX
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14-JUL-2000

26-JUL-2000

26-JUL-2000

14-AUG-2000

11-AUG-2000

11-AU
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19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JAN-2001;
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                                                                                                                                                   2000US-0225758.
2000US-0225759.
2000US-0226279.
2000US-0226681.
2000US-0226868.
2000US-0227182.
2000US-0227109.
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2000US-0225270.
2000US-0225447.
2000US-0225757.
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2000US-0225266.
2000US-0225267.
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2000US-0224518.
2000US-0224519.
2000US-0225213.
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2000US-0218290.
2000US-0220963.
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2000US-0215135.
2000US-0216647.
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2000US-0198123.
2000US-0205515.
2000US-0209467.
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                                                                                         2000US-0228924
2000US-0229287
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2000US-0217487
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08-SEP-08-SEP-08-SEP-08-SEP-

5-SEP-2000; 5-SEP-2000; 5-SEP-2000; 5-SEP-2000; 8-SEP-2000;

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                                                                                                                                                                    Query Match
Best Local S
Matches 219
                                                                                                                                                                                                                                                                 associated with aberrant calcium flux. Such disorders include neurological diseases (e.g. amylotrophic lateral sclerosis, ALS), immune dysfunction (e.g. severe combined immunodeficiency, SCID), digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or infectious disease (e.g. acquired immunodeficiency syndrome, ALDS). The novel calcium-binding proteins are also useful as screening tools to identify antagonists and/or agonists that may enhance or inhibit activities mediated by calcium-binding proteins. The polynucleotides of the invention are also useful in gene therapy. AAU19992-AAU19999 represent the novel human calcium-binding proteins.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fire, wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-NOV-2000
01-DEC-2000
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated
used in p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to the isolation of novel human calcium-binding proteins, and (AR331577-AR331654) and genomic sequences encoding for these proteins. The sequences of the inventage are useful in the diagnosis, prevention and/or prognosis of disease
                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                            121
                                                                                                                                                                    Local Similarity
nes 219; Conserv
                                                        74
                                                                                  61
                                                                                                               14
                                                                                                            2001-465568/50.
DB; AAS31626.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID No 138; 542pp; English.
                                                                                                                                                                  46.1%;
nilarity 94.8%;
Conservative
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2000US-0249217
2000US-0249218
2000US-0249244
2000US-0249265
2000US-0249264
2000US-0249269
2000US-0249299
2000US-0249299
2000US-0250316
2000US-0251030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid molecule encoding a can
ng, treating or ameliorating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SC,
                                                                                                                                                                    Score 1143; DB 22;
Pred. No. 2.7e-96;
0; Mismatches 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a calcium-binding ating a medical cor
                                                                                                                                                                                                                                                                                   ot form part of the printed format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        medical condition
                                                                                                                                                                     Indels
                                                                                                                                                                                               Length 244;
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diseases
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  193
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2000US-0229509
2000US-0229509
2000US-0230438
2000US-0231243
2000US-0231241
2000US-0231241
2000US-0231241
2000US-0232080
2000US-0232397
2000US-0232397
2000US-0232397
2000US-0232397
2000US-0232397
2000US-02332400
2000US-02332401
2000US-02332401
2000US-02332401
2000US-02332401
2000US-0234297
2000US-0234297
2000US-0234299
2000US-0234299
2000US-0234299
2000US-0236369
2000US-0246478
2000US-0246478
2000US-0246610
2000US-0246610
2000US-0246611
2000US-0249201
2000US-0249211

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AAB50388
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Best Local S
Matches 181
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08-JUL-1999;
18-AUG-1999;
12-NOV-1999;
                                                                                                                                                                                             or research purposes. The uncoupling protein encoded by the nucleotide sequences may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders, wounds, infectious diseases, thrombosis, arthritis, and infertility.
                                                                                                                                                                                                                                                           The present sequence is a human uncoupling protein. The nucleotide sequences encoding the uncoupling proteins may be used for the detection of various disorders such as cancer, for chromosome identification, as chromosome markers and for numerous other diagnostic
                                                                                                                                                                                                                                                                                                                                                Uncoupling proteins and nucleic acid sequences encoding them, useful for detecting, preventing and treating proliferative, neurological, immune system, cardiovascular and gastrointestinal disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antirheumatic; antiproliferative; cardiant; vasotropic; cerebroprotective; neuroprotective, antipacterial; opthalmological; gastrointestinal; nephrotropic; gynaecological; vulnerary; thrombolytic; gene therapy; cancer; wound; infectious disease; thrombosis; arthritis;
                                                                                                                                                                                           thrombosis, arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAC90462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human uncoupling protein #11.
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                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                           Claim 11; Page 328-329; 343pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-656322/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; uncoupling
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                            200
                                                                              140
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AGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFROMVKEGGIRSLWRGNGTNVI 259
                                                                             MTVDWNEWRDYFLFNPVTDIEEIIRFWKHSTGIDIGDSLTIPDEFTEDEKKSGQWWRQLL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                           SM,
                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
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                                                                                                                                                                        292 AA;
                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENOME
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99US-0142821.
99US-0149448.
99US-0164751.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; immunosuppressive; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein; 292
                                                                                                                41.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCI INC.
                                                                                                        53;
                                                                                                      Score 1037; D: Pred. No. 1.8e
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                                                                                                                 DB 21;
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           SVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQA 417
                                     kiapesaikfmayeqikrailgqqetlhvqerfvagslagataqtiiypmevlktrltlr 180
                                                                                          KIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIYPMEVMKTRLAVG 319
sadpgilvllacgtisstcgqiasyplalvrtrmqaqa
 278
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Search completed: August 18, Job time: 3814 sec 2002, 09:22:20 THIS PAGE BLANK (USPTO)

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Result
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1

2: /cgn2_6/ptodata/1

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US-09-234-613-12
US-09-160-119-2
US-09-160-119-2
US-09-234-613-19
US-08-933-750C-19
US-09-234-613-19
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| EEKIF KQKIV LTISE :- - | 1 18-930-339 18-930-339 100 6150502 100 6150502 101 1070XMATION: CLANT: Watson, CCANT: Strachan CCANT: Strachan CCANT: Murison, OF INVENTION: OF INVENTION: OF INVENTION: OF INVENTION: OF INVENTION: OF EQ ID NOT REFERENCE: 110 NAT APPLICATION: OF SEQ ID NOT THE HOST OF SEQ ID NOT ARE: FastSEQ f NO 339 19 PRT NO 339 19 PRT NO 339 19 PRT MATCH MA | 224 224 224 198.5 198.5 198.5 198.5 198.5 193.5 193.5 193.5 193.5 179 179 179 |
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| NNDGKIEASEIVQSLQTLG 119 | n Cells Length 469; Indels 0; Gaps 0; | Sequence 2, Appli Sequence 2, Appli Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 56, Appl Sequence 56, Appl Sequence 56, Appl Sequence 56, Appl Sequence 56, Appl Sequence 6, Appli Sequence 6, Appli |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 142 LENCTH: 312 TYPE: PRT
                                                                                                                                                                                                                              Sequence 10, Appli
Patent No. 6013858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 348
                             TITLE OF INVENTION: Mouse Lacking Heart-Muscle A
TITLE OF INVENTION: Nucleotide Translocator Prot
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                             APPLICANT: Wallace, Douglas C. APPLICANT: Graham, Brett H. APPLICANT: MacGregor, Grant R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        | QMVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAG
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                   Boulder
                                                                                                                                                                                                                                             Application US/08961871
Colorado
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63.2%;
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Pred. No. 1e-80;
                                                                                                                             Heart-Muscle Adenine
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                                                                                                              Protein
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                                                                                                                                                                                                                                                                                                       ; Sequence 15, Application US/09068140A
; Patent No. 6281409
                                                                                                                                                                                                                                                                                    Patent No. 6281409
GENERAL INFORMATION:
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Best Local Similarity 32.3
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (303) 499-80 INFORMATION FOR SEQ ID NO:
COUNTRY: USA
ZIF: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                          APPLICANT: Mary Rose Woodhead, Mark Andrew Taylor APPLICANT: and Rex Michael Brennan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                    TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                     ADDRESSEE: 5...
                                                                                                                                                                                                                                                                                                                                                                                                                              245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 RQLLAGGIAGAVSRTSTAPLDRLKIMMQV-HGSK---SDKM--NIFGGFRQMVKEGGIRS 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360 IDLAVYELLKSYWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAML 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linon
                                                                                                  STREET: 709 Swedeland CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ferber, Donna M. REGISTRATION NUMBER: 33 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 KDFLAGGIAAAVSKTAVAPIERVKLLLQVQHASKQISAEKQYKGIIDCVVRIPKEQGFLS 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 31-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGSPQL--NMVGLFRRIISKEGIPGLYRGITPNFMKVLPAVGISY--VVYENMKQ 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AYFGVYDTAK-----GMLPDPKNVHIIVSWMIAQSVTAVAGLVSYPFDTVRRRMMQSGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDRHKQFWRYFAGNLASGGAAGATSLC 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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9 Swedeland
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                                                                                                                                                                                                    Blackcurrant Promoters and Genes: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.0%; Score 347; DB 3 32.2%; Pred. No. 1e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/961,871
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                                                                                                                                            Beecham Corporation Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Length 298;
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US-09-068-140A-10
; Sequence 10, Application US/09068140A
; Patent No. 6281409
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                   RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVOIDETICAL: YES
ANTI-SENSE: NO
ANTI-SENSE: No-terminal
                                                             TITLE OF INVENTION: Blackcurrant Promoters and Genes
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE: I
ORIGINAL SOURCE:
ORGANISM: Rib
                                                                                                                                      APPLICANT: Mary Rose Woodhead, Mark Andrew Taylor APPLICANT: and Rex Michael Brennan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/EP96/04807 FILING DATE: No. 6281409ember 4, 1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/EP96/04807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/068,140A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5017
                                                                                                                                                                                                                                                                                                                                        424 QLNMVGLFRRIISKEGIPGLYRGITPNFMKVLPAVGISYVVYENMK 469
                                                                                                                                                                                                                                                                                                                                                                               210
                                                                                                                                                                                                                                                                                                                                                                                                                 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 QWWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQ----MVKEGGIR 248
                                 CITY:
                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Dinner, Dara L.
REGISTRATION NUMBER: 33,680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                        IQDVIG---SIVKKNGYVGLMRGWIPRMLFHAPAAAICWSTYEASK 312
                                                                                                                                                                                                                                                                                                                                                                                                KSYWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAM-----LEGSP 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MDVVKQRLQL-QSSPYKGVVDCVRRVLVEEGIGAFYASYRTTVVMNAPFTAVHFATYEAT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYELL 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLYRGIGAMGLGAGPAHAVYFSVYEMCKETFS-HGDPSNSGAHAVSGVFATVASDAVITP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIYP 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QFWQFMIAGSIAGSIEHMAMYPVDTLKTRIQGIGSCSAQS---AGLRQALGSILKVEGPA 91
                                                                                                                                                                                                                                                                                                                                                                           KKGLLEVSPETANDENLLVHATAGAAAGALAAVVTTPLDVVKTQLQCQGVCGCDRFSSSS 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
85; Conserv
                          King of Prussia
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                PΑ
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PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
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29.7%;
                                                  Road
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Pred. No. 2.3e-23;
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US-08-933-750C-12

Sequence 12, Application US/08933750C Patent No. 5932442

GENERAL INFORMATION:

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

Lal, Preeti
Hilman, Jennifer L.
Bandman, Olga
Shah, Purvi
Au-Young, Janice
Yue, Henry

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APPLICATION NUMBER: PCT/EP96/048
FILING DATE: No. 6281409ember 4,
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: NO ANTI-SENSE: NO
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: KILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
236
                                429
                                                                176
                                                                                                                               117
                                                                                                                                                                                                                                                                                          198 LLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQ----MVKEGGIRSLWRG 253
                                                                                                                                                          314 TRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYELLKSYWL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Dinner, Dara L. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                            1 MIAGSIAGSIEHMAMYPVDTLKTRIQAIGSCSAQS---AGLRQALGSILKVEGPAGLYRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 289 amino acids
G---SIVKKNGYVGLMRGWIPRMLFHAPAAAICWSTYEASK 273
                           GLFRRIISKEGIPGLYRGITPNFMKVLPAVGISYVVYENMK 469
                                                             EVSPETANDENLLVHATAGAAAGALAAVVTTPLDVVKTQLQCQGVCGCDRFSSSSIQDVI
                                                                                                                                                                                                                           NGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIYPMEVMK 313
                                                                                           DNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAM~~~~-LEGSPQLNMV
                                                                                                                              QRLQL-QSSPYKGVVDCVRRVLVEEGIGAFYASYRTTVVMNAPFTAVHFATYEATKKGLL
                                                                                                                                                                                             IGAMGLGAGPAHAVYFSVYEMCKETFS-HGDPSNSGAHAVSGVFATVASDAVITPMDVVK
                                                                                                                                                                                                                                                                                                                              83;
                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                              Conservative
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YES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                            12.6%; Score 311.5; 29.5%; Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10:
                                                                                                                                                                                                                                                                                                                            51;
                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                             No. 2.8e-22;
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                                                                                                                                                                                                                                                                                                                                                         DB 4;
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                                                                                                                                                                                                                                                                                                                                                           289;
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В
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
LIBRARY: SPLNNOT02
CLONE: 207452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/933,7
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: CORLEY, Neil C.
HUMAN R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
300 FFSYE 304
                                                                                                                                                                                                                                                     121 HFVCGGLAACMATLTVHPVDVLRTRFAAQGEPKVYNTLRHAVGTMYRSEGPQVFYKGLAP 180
                                     462 YVVYE 466
                                                                               240 FKKRLQVGGFEHARAAFGQVRRYKGLMDCAKQVLQKEGALGFFKGLSPSLLKAALSTGFM 299
                                                                                                                                                                                                                                                                                                                                                                              239 -- ROMVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFE----- 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 DEKKSGQ----WWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHG---SKSDKMNIFGGF-- 238
                                                                                                                                                                                                                                                                                                                                        65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
SOFTWARE: FastSEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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                                                                                                                                                                   TLIAIFPYAGLQFSCYSSLKHLYKWAIPAEGKKNENLQNLL-CGSGAGVISKTLTYPLDL
                                                                                                                                                                                                           NLLGIIPYAGIDLAVYELLKS-YWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLAL 408
                                                                                                                                                                                                                                                                                            RFISGSMAGATAQTFIYPMEVMKTRLAV-GKTGQYSGIYDCAKKILKHEGLGAFYKGYVP 349
                                                                                                                                                                                                                                                                                                                                      ASRQILQEEGPTAFWKGHVPAQILSIGYGAVQFLSFE----MLTELVHRGSVYDAREFSV 120
                                                                                                                       VRTRMQAQAMLEGSPQLNMV----GLF---RRIISKEGIPGLYRGITPNFMKVLPAVGIS 461
                                                                                                                                                                                                                                                                                                                                                                                                                        DPKPDGRNNTKFQVAVAGSVSGLVTRALISPFDVIKIRFQLQHERLSRSDPSAKYHGILQ 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84;
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Pred. No. 1.4e-20;
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US-09-234-613-12
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Patent No.
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REG
NUMBER OF SEQUENCES: 98
                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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                                350 NLLGIIPYAGIDLAVYELLKS-YWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLAL 408
                                                                     121
                                                                                                     291 RFISGSMAGATAQTFIYPMEVMKTRLAV-GKTGQYSGIYDCAKKILKHEGLGAFYKGYVP 349
                                                                                                                                                                          239 --RQMVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFE----- 290
                                                                                                                                                                                                                                             187 DEKKSGQ---WWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHG---SKSDKMNIFGGF--
                                                                                                                                          65
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM COR
OPERATING SYSTEM:
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TLIAIFPYAGLQFSCYSSLKHLYKWAIPAEGKKNENLQNLL-CGSGAGVISKTLTYPLDL 239
                                                                     HFVCGGLAACMATLTVHPVDVLRTRFAAQGEPKVYNTLRHAVGTMYRSEGPQVFYKGLAP 180
                                                                                                                                          ASRQILQEEGPTAFWKGHVPAQILSIGYGAVQFLSFE----MLTELVHRGSVYDAREFSV 120
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Bandman, Olga
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                                                                                                                                                                                                                                                                                Score 295; DB 4;
Pred. No. 1.4e-20;
61; Mismatches 130
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CURRENT APPLICATION NUMBER: US/09/160,119A
CURRENT FILLING DATE: 1998-09-24
EARLIER APPLICATION NUMBER: E9 97402511.6
EARLIER FILLING DATE: 1997-10-23
EARLIER APPLICATION NUMBER: EP 98401655.0
EARLIER FILLING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 4
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 674
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Patent No. 6316219
GENERAL INFORMATION:
APPLICANT: KRIEF, STEPHANE
APPLICANT: SOUCHEF, MICHEL
APPLICANT: BRIL, ANTOINE
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30985
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Best Local Similarity
Matches 121; Conserv
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                                                                                                                                 IRLQV--AGEITTGPRVSALSVVRDLGFFGIYKGAKACFLRDIPFSAIYFPCYAHVKA--
                                                                                                                                                                                                LLPQLLGVAPEKAIKLTVNDFVRDKFMHKDGSVPLAAEILAGGCAGGSQVIFTNPLEIVK
                                                                                                                                                                                                                                                                                                                                  EQ-----FINPYTDIEEIIR 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QFLLEIQLEHAKQAFVQRDNARTGRVTAIDFRDIMVTIRPHVLTPFVEECLVAAAGGTTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FQLFDKAGKGEVTFEDVKQVFGQTTIHQHIPFNWDSE---FVQLHFGKERKRHLTYAEFT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FQALDRNGDGVVDIGELQE -- GLRNL -- GIPLGQDAEEKIFTTGDVNKDGK -- LDFEEFM 81
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                             FRRIISKEGIPGLYRGITPNFMKVLPAVGISYVVYENMKQ 470
                                                               --SFANEDGQVSPGSLLL--AGAIAGMPAASLVTPADVIKTRLQVAARAGQTTYSGVIDC
                                                                                              LDNFAKD--SVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLEGSPQLNMVGL
                                                                                                                                                                                                                                  NGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIYPMEVMK
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US-08-933-750C-19

Sequence 19, Applicat Patent No. 5932442 GENERAL INFORMATION:

9, Application US/08933750C 5932442

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

Lal, Preeti Hillman, Jennifer Bandman, Olga

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APPLICANT: APPLICANT: APPLICANT:

Shah, Purvi Au-Young, Janice Yue, Henry Guegler, Karl J. Corley, Neil C.

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US-09-160-119-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/160,119A CURRENT FILING DATE: 1998-09-24 EARLIER APPLICATION NUMBER: EP 97402511.6 EARLIER FILING DATE: 1997-10-23
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APPLICANT: BRIL, ANTOINE.
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30985
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344
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                                                                                      286
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                                                                                                                                                                                                           KTGQY-SGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYELLKSYWLDNFAK 378
                                                                                                                                                                                                                                                                                        KIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIYPMEVMKTRLAVG
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                                         KEGIPGLYRGITPNFMKVLPAVGISYVVYENMKQ 470
                                                                                                                             D--SVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLEGSPQLNMVGLFRRIIS
                                                                                                                                                                        -AGEITTGPRVSALSVVRDLGFFGIYKGAKACFLRDIPFSAIYFPCYAHVKA----SFAN
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EEGPKALWKGAGARVFRSSPQFGVTLLTYELLQR
                                                                                  EDGQVSPGSLLL---AGAIAGMPAASLVTPADVIKTRLQVAARAGQTTYSGVIDCFRKILR
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Sequence 19, Application US/09234613
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Best Local S
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SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS
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                                                                                                                            441 PGLYRGITPNFMKVLPAVGISYVVYE-----NMKQTLG 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 QQMVASGTGAVVTSLFMTPLDVVKVRLQSQRPSMASELMPSSRLWSLSYTKWKCLLYCNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 79; Conserv
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SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                                                                               KFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIYPMEVMKTRLAVGKTGQYSGI 327
                                                                                                                                                                                                                                                                                                                                                                                   VLEPLYLCPNGARCATWFQDPTRFTGTMDAFVKIVRHEGTRTLWSGLPATLVMTVPATAI 132
                                                                                                                                                               FV--AGGISGTVAAVLTLPFDVVKTQRQVALGAMEAVRVNPLHVDSTWLLLRRIRAESGT
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                                                                                         KGLFAGFLPRIIKAAPSCAIMISTYEFGKSFFQRLNQDRLLG
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ber 23, 1997
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GENERAL INFORMATION:
APPLICANT: Lal, P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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FILING DATE: September 2:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,7
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APPLICANT: Corley, Neil C.
ATTILE OF INVENTION: HUMAN RI
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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387 VILGCGALSSTCGQLASYPLALVRTRMQAQAMLEGSPQLNMVG-----LFRRIISKEGI 440 : | :| | : | :| : | | | | | :: |
                                                      192 GACVRTAVAQGGWRSLWLGWGPTALRDVPFSALYWFNYELVKS-WLNGLRPKDQTSVGMS 250
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                                                                                                                                                                                                      73 VLEPLYLCPNGARCATWFQDPTRFTGTMDAFVKIVRHEGTRTLWSGLPATLVMTVPATAI 132
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CLONE: 724157
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                                                                                                                                                                                                                                                                              QQMVASGTGAVVTSLFMTPLDVVKVRLQSQRPSMASELMPSSRLWSLSYTKWKCLLYCNG 72
                                                                                      YDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYELLKSYWLDNF-AKDSVNPGVM 386
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Bandman, Olga
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Best Local :
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APPLICATION NUMBER: US/08/775,009
FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 311 amino acids
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NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CH-0681
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MEDIUM TYPE: Floppy disk
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207
                                370 SYWLDNFAKDSVNP---GVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLEGSPQLN
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TOPOLOGY: lin
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                                                                                                                                                    LSSLLYGSIPKAAVRFGMFEFLSNHMRDAQGRLDSTRGLLCGLGAGVAEAVVVVVCPMETV 146
                                                                                                             KTRLAVGKTG---QYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYELLK 369
NWYRGDNPNKPMNPLITGVF-----GAIAGAASVFGNTPLDVIKTRMQG----LEAHKYRN
                                                                        KVKFIHDQTSPNPKYRGFFHGVREIVREQGLKGTYQGLTATVLKQGSNQAIRFFVMTSLR
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E: No. 5935783ris, LLP
One Liberty Place - 46th Floor
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                   Length 311;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TELEFAX: 66141
                                   421 ----GSPQLNMVGLFRRIISKEGIPGLYRGITPNFMKVLPAVGISYVVYENMKQTL 472
                                                                                                                                              126 PTDVVKVRFQAQARAGGGRRYQSTVNAYKTIAREEGFRGLWKGTSPNVARNAIVNCA--E 183
                                                                                                                                                                                                                                                            248 RSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIY 307
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 240 YSSAGHCALTM-----
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SOFTWARE: Patentl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036-2711
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STATE: New Yor
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                                                                                            LAVYELLKSYWLD-NEAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLE
                                                                        LVTYDLIKDALLKANLMTDDLPCHFTSAFGAG----FCTTVIASPVDVVKTRYMNSALGQ
                                                                                                                                                                                    PMEVMKTRL-AVGKTG---QYSGIYDCAKKILKHEGLGAFYKGYVPNLL--GIIPYAGID 361
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I: U.S.A.
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VENTION: COMPOSITIONS AND METHODS FOR THE
VENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                           9.48;
-LQKEGPRAFYKGFMPSFLRLGSWNVVMFVTYEQLKRAL
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Pred. No. 1.3e-14;
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RESULT 15
US-08-518-878B-51
; Sequence 51, Application US/08518878B
; Patent No. 5702902
; GENERAL INFORMATION:
    APPLICANT: Tartaglia, Louis A.
    APPLICANT: OF INVENTION: COMPOSITIONS A)
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: COTUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-0031-999
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tartaglia, Louis C.
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Treatment of Body Weight Disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 QLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKM-----NIFGGFRQMVKEGGI 247
                                                                                                                                                                                                                    421
                                                                                                                                                                                                                                                                                                                           126
                                                                                                                                                                                240 YSSAGHCALTM------LQKEGPRAFYKGFMPSFLRLGSWNVVMFVTYEQLKRAL 288
                                                                                                                                                                                                                                                     184 LVTYDLIKDALLKANLMTDDLPCHFTSAFGAG----FCTTVIASPVDVVKTRYMNSALGQ
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Local Similarity 25.3%;
hes 75; Conservative 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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No. 5861485
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212) 869-8864
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                COMPOSITIONS AND METHODS
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Pred. No. 1.3e-14;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amin
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                       16 KFLGAGTAACIADLITFPLDTAKVRLQIQGESQGPVRATVSAQYRGVMGTILTMVRTEGP 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                 LAVYELLKSYWLD-NFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLE 420
                                     ----GSPQLNMVGLFRRIISKEGIPGLYRGITPNFMKVLPAVGISYVVYENMKQTL 472
                                                                                                                                                                                  PMEVMKTRL-AVGKTG---QYSGIYDCAKKILKHEGLGAFYKGYVPNLL--GIIPYAGID 361
YSSAGHCALTM-----LQKEGPRAFYKGFMPSFLRLGSWNVVMFVTYEQLKRAL 298
                                                                           LVTYDLIKDALLKANLMTDDLPCHFTSAFGAG----FCTTVIASPVDVVKTRYMNSALGQ
                                                                                                                                                      PTDVVKVRFQAQARAGGGRRYQSTVNAYKTIAREEGFRGLWKGTSPNVARNAIVNCA--E
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| | | XWNC | S29852 | S31814 | XWBO | T09709 | S33630 | A29132 | A31978 | A41677 | A44778 | S17917 | S37210 | A24849 | S68154 | S16568 | TPOT/3 |
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ALIGNMENTS

RESULT T50686

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c; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C; Accession: T22688
R; Kershaw, J.
submitted to the EMBL Data Library, May 1996
A; Reference number: Z19600
A; Accession: T22688
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-588 <WIL>
A; Cross_references: EMBL: Z72511; PIDN: CAA96658.1; GSPDB:GN00023; CESP:F55All
A; Cross_references: EMBL: Z72511; PIDN: CAA96658.1; GSPDB:GN00023; CESP:F55All
protein F17E5.2 [imported] - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text C;Accession: G89667 R;anonymous, The C. elegans Sequencing Consortium. Science 282, 2012-2018, 1998 A;Title: Genome sequence of the nematode C. elegans: a pA;Title: Genome sequence wustl.edu/gsc/C_elegans/ and A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and A;Note: published errata appeared in Science 283, 35, 19
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A; Map po
A; Intron
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LQNEGYTGFYRGITPNFLKVIPAVSISYVVYEKVRTGLGV
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04; Mismatches
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3.9e-65;
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283, 2103, 1999; an
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A;Map position: X
A;Introns: 21/1; 48/:
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A; Accession: T21074
A; Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F17E5.2 - Caenorhabditis elegans C;Specles: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t. C;Accession: T21074
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A; Status: prellminary
A; Molecule type: DNA
A; Residues: 1-531 <STO>
A; Cross-references: GB:chr_X;
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A;Gene: F17E5.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVPEDFTPQELLSGVWWRHLVAGGVAGAMSRTCTAPFDRIKVYLQVMYLHLLFHIMFLKA
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     EQPTRYETLFQALDRNGDGVVDIGELQEGLRNLGIPLGQDAEEKIFTTGDVNKDGKLDFE 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLGAFYKGYVPNLLGIIPYAGIDLAVYELLKSYWLDNFAKDSVNPGVMVLLGCGALSSTC
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                                                                                                                             21/1; 48/3;
                                                          Similarity
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Z19368
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42.3%;
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                                      91;
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                                        Score 988.5;
Pred. No. 1.4e
91; Mismatches
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Pred. No. 7.7e-58;
2; Mismatches 138;
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                                                       988.5;
No. 1.4
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                                        137;
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18-Feb-2000

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428 398 338 309

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Gaps

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CESP: F17E5

Вb

209

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A;Cross-references: EMBL:A
A;Experimental source: cul
C;Genetics:
A;Gene: ATSP:TZ11.30
A;Map position: 5
A;Introns: 133/1; 391/1; 4
C;Keywords: peroxisome
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749871
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jun-2000
C:Accession: 749871
R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24493
A:Accession: 749871
A:Scatus: preliminary
A:Accession: T49871
A:Scatus: preliminary
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A; Residues: 1-479 <BEV>
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                                                                       TMTVDWNEWRDYFLFNP-VTDIEEIIRFWKHSTGIDIGDSLTIPDEFTEDEKKSGQWWRQ
                        LLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQMVKEGGIRSLWRGNGTN
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mitochondrial solute carrier protein homolog - Arabidopsis thaliana N;Alternate names: protein A_IG002N01.16 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 19-Reb-1999 #sequence_revision 19-Reb-1999 #text_change 24-Nov-1999 C;Accession: T01729 R;Scheet, P.; Maggi, L. submitted to the EMBL Data Library, June 1997 A;Bescription: The sequence of A. thaliana IG002N01. A;Reference number: Z14407 A;Reference number: Z
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A;Molecule type: DNA
A;Residues: 1-352 <SCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIYPMEVMKTRL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLAGGLAGAVSRTATAPLDRLKVVLQVQRAHA---GVLPTIKKIWREDKLMGFFRGNGLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 521; DB 2; Pred. No. 4.9e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                   273
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hypothetical protein F5K20.240 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 17-Mar-2000 C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 17-Mar-2000 C;Accession: T45934 R;Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Mewes, H.W.; Lemcke, K.: 1
A;Map position: 3
A;Introns: 98/3; 157/3; 207/3; 234/3; 258/2; 281/1
A;Note: F5K20.240
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier
                                                                                                                                                                                 A; Reference number: Z23017
A; A; Accession: T45934
A; Accession: T45934
A; Ctarran
                                                                                                                                                                                                                                                                                                                                                  RESULT
T45934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Benes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, submitted to the Protein Sequence Database, Marcl A;Reference number: 224473
A;Accession: T47703
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ca-dependent solute carrier-like protein - Arabidopsis thaliana N;Alternate names: protein F1116.50 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 08-Sep-2000 C;Accession: T47703 T47703 R;Benes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Lemcke, K
                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 3
A;Introns: 63/3; 122/3; 172/3; 206/3; 230/2; 253/1
A;Note: F1I16.50
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier
                                                                            A; Experimental source: C; Genetics:
                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-358 <MON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: cultivar Columbia; BAC C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: EMBL: AL161667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-332 <BEN>
                                                                                                                  A; Cross-references:
                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYELLKSYWLDNFAKDSVNPGVMVLLGCGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GMENHKEGISSNLFVHFVAGGLAGITAASATYPLDLVRTRLAAQTKVIYYSGIWHTLRSI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGIASSTATFPLDLVRRRKQ----LEGIGGRAVVYKTGLLGTLKRIVQTEGARGLYRGIL 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSTCGQLASYPLALVRTRMQAQAMLEGSP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTDEGILGLYKGLGTTLVGVGPSIAISFSVYESLRSYWRSTRPHDS----PIMVSLACGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNAAALRKPSILHEASRILNEEGLKAFWKGNLVTIAHRLPYSSVNFYAYEHYKKFMYMVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SD----KMNIFGGFRQMVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQYKKLL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSGHGVASS---SHRLTQDQRSHIESASQLLAGGLAGAFSKTCTAPLSRLTILFQVQGMH
                                                                                                                                                                                                                                                                                                                                                                                                                             PEYYKVVPGVGICFMTYETLK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PNEMKVLPAVGISYVVYENMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----TEEGQKIGTFERFISGSMAGATAQTFIYPMEVMKTRLAV-GKTGQYSGIYDCAKKI 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                              EMBL:AL132960
pe: cultivar Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 520; DB 2; Pred. No. 5.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                BAC
                                                                                                                                                                                                                                  January
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           March
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -QLNMVGLFRRIISKEGIPGLYRGIT 448
                                                                                                clone F5K20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone F1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000
                                                                                                                                                                                                                                    2000
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   protein repeat homology
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                                                                                                                                                                                                                                                    K.; Mayer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245
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                                                                                                                                                                                                                                                      K.F.X
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                                                                                                                                                                                                                                                                                                         QΥ
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A; Introns: 54/3; 426/2
C; Keywords: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: T39385
R;Lyne, M.; Rajandream, M.A.;
submitted to the EMBL Data Lil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QΥ
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   20
                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-500 <LYN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: T39385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  429
                                                                                                                                                                                              148
                                                                                                                                                                                                                                  215
                                                                                                                                                                                                                                                                                         166 WKHST------GIDIGDSLTIPDEFTEDEKKSGQWWRQLLAGGIAGAVSRTSTAP 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           145
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     382
                                           268
                                                                                                                                                                                                                                                                     96 WIHDTPHMKLVFHRLQNLPDGDLL-----LENDPKNNVGY--FISGGIAGIVSRTCTAP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25
                                                                                                                                                                                                                                                                                                                                                                      Local
                                         QYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYELLKSYWLDNFA-KDSV 381
                                                                                                                                                       WAYEQYKKLL--TEEGQKIGTFERFISGSMAGATAQTFIYPMEVMKTR-----LAVGKTG 322
                                                                                                                                                                                                                    LDRLKIMM-QVHGSKSDKMNIFGGFRQMVK----EGGIRSLWRGNGTNVIKIAPETAVKF 269
                                                                                                                    GTYEAMKRVLGISSSSENHSPLYSYLAGGMAGSVAQMFIYPVDTLKFRIQCSDLSRGQHG
   NPGVM-----VLLGCGALSSTCGQLASYPLALVRTRMQAQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HRPNDS
                                                                                                                                                                                          LDRLKVMLISDTGSKPSPKYPFATLLHTTKVLWNRNGIRSFFVGNGINVLKVMPESSIKF
                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                    20.2%;
35.8%;
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168 HSTGIDIGDSLTIPDEFTEDEKKSGQWWRQ------LLAGGIAGAVSR 209
GTFKHIFKTEGMRGLYRGIIPEYYKVVPGVGIAFMTFEELKKLL
                                                                                                                                                                                                                                                                                                                              GAVNFYAYEEYKTFLHSNPVLQSYKGNAGVDISV--HFVSGGLAGLTAASATYPLDLVRT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSTAPLDRLKIMMQVHGSKSD-----KMNIFGGFRQMVKEGGIRSLWRGNGTNVIKIAPE 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HNTVVDAGNRKLLQQQPQTQQTQSCHQHHQSNKQSLNQQQGHFGTVERLLAGGIAGAFSK 84
                                                GLFRRIISKEGIPGLYRGITPNFMKVLPAVGISYVVYENMKQTL
                                                                                                                                                            NFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLEGSP----
                                                                                                                                                                                                                                                                           RLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYELLKSYWLD 374
                                                                                                                                                                                                                                                                                                                                                          TAVKFWAYEQYKKLLTEE------GKIGTFERFISGSMAGATAQTFIYPMEVMKT 314
                                                                                                                                                                                                                       RLSA-----QGVGHAFRTICREEGILGLYKGLGATLLGVGPSLAISFAAYETFKTFWLS 256
                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTAPLARLTILFQIQGMQSEAAILSSPNIWHEASRIVKEEGFRAFWKGNLVTVAHRLPY 144
                                                                                                           -- NAVVSLGCGSLSGIVSSTATFPLDLVRRRMQ----LEGAGGRARVYTTGLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 506; DB 2;
Pred. No. 4.9e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                 -QLNMV 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                           309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
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probable mitochondrial carrier protein - fission yeast (Schizosaccharomyces C;Species: Schizosaccharomyces pombe C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000 C;Accession: T39385 A;Cross-references: EMBL:AL035085; PIDN:CAA22679.1; A;Experimental source: strain 972h-; cosmid c12D12 SPDB:SPBC12D12.05c Z21850 A.; Barrell, B.G.; Xiang, Library, January 1999 Z.; GSPDB:GN00067; SPDB:SPBC12D12.05c Aves, pombe)

63;

Mismatches 109;

Indels

Gaps

12;

AMLEGSPQLNMVGL 430

267

207

Score 500.5; DB 2; Pred. No. 1.8e-25;

Length

500; 49;

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submitted to the EMBL Data Library, May 1992
A; Description: Sequence and pattern of expression of a bo A; Reference number: $26596
A; Accession: $26596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: GDC

G;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology C;Keywords: cardiac muscle; duplication; heart; mitochondrion; transmembrane prof;31-119/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;125-215/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;235-327/Domain: ADP,ATP carrier protein repeat homology <ACP3>
                                                                                                                                                                                                                        RESULT
D84798
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                                                                                                        probable mitochondrial carrier protein [imported] - Arabidopsis
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change
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DNA Seq. 3, 71-78, 1992
A;Title: Sequence and pattern of expression
A;Reference number: 146022; MUID:93091248
A;Accession: 146022
                                        R; Lin, X.;
                                                                          C; Accession: D84798
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A;Residues: 1-330 <FIE>
A;Cross-references: EMBL:X66035; NID:g386; PIDN:CAA46834.1;
A:Cross-references: EMBL:X66035; NID:g386; PIDN:CAA66834.1;
A:Cross-references
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                                            Kaul, S.;
       Moffat,
Rounsley, S.D.; Shea, K.S.; Cronin, L.A.; S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.48;
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   Shen, M.;
                                        T.P.;
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                                     Benito,
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   VanAken, S.E.;
                                                                                                        #text_change 16-Feb-2001
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                                     M.I.;
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                                 Town, C.D.;
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   Umayam, L.;
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       Tallon,
   C.Y.;
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A;Cross·references: GB:AE002093;
C;Genetics:
A;Gene: At2g37890
A;Map position: 2
C;Superfamily: ADP,ATP carrier p:
C;Keywords: mitochondrion
                                                                                                                                                                                                                                                                    hypothetical protein F7A7.20 - Arabidopsis thaliana (Species: Arabidopsis thaliana (Mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 C;Accession: T48171 N; Ardiles, W; Buysshaert, C, R;Bevan, M; Terryn, N; Ardiles, W; Buysshaert, C, ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X. submitted to the Protein Sequence Database, March 20
                                                                                A; Map position: 5
A; Introns: 144/3;
A; Note: F7A7.20
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A;Molecule type: DNA
A;Residues: 1-348 <ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Sequence and analysis of chromosome A; Reference number: A84420; MUID:20083487 A; Accession: D84798
                                                                                                                                  A; Experimental C; Genetics:
                                                                                                                                                                   A; Cross-references:
                                                                                                                                                                                     A; Molecule type: DNA A; Residues: 1-415 <BEV>
                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                    A; Reference number: A; Accession: T48171
Query Match
Best Local S
Matches 107
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Best Local
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 107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YVVYENMKQTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FWKGNLVTVVHRIPYTAVNFYAYEKYNLFFNSNPVVQSFIGNTSGNPIVHFVSGGLAGIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVRRRMQ-----VEGAGGRARVYNTGLFGTFKHIFKSEGFKGIYRGILPEYYKVVPGVGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVRTRMQAQAMLEGSP-----QLNMVGLFRRIISKEGIPGLYRGITPNFMKVLPAVGIS
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                 Similarity
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 Conservative
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                                                                                                  163/3;
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                                                                                                                                            EMBL:AL161946
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                                                                                                                                                                                                                                                                  Lemcke, K.;
ein Sequence
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            18.4%;
                                                                                                  184/3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
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 66;
                                                                                                  203/3;
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Pred. No. 5.2e-24;
2; Mismatches 103
            Score 455.5;
Pred. No. 1.3
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Mismatches
                                                                                                  231/3;
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            1.3e-22;
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115;
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35;
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Gaps
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-LLAGGIAGAVSRTSTAPLDRLKIMM 222

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hypothetical protein F20B18.290 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein [imported] - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 28-Jul-2000
C; Accession: T51158
R; Comella, P.; Wu, H.J.; Laudie, M.; Berger, C.; Cooke, R.; Delseny, M.; Grellet, F.
Plant Mol. Biol. 41, 687-700, 1999
A; Title: Fine sequence analysis of 60 kb around the Arabidopsis thaliana AtEml locus
                                                           RESULT
T04273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ A;MoLecule type: DNA A;Residues: 1-381 <COM> A;Cross-references: EMBL:AF049236; PIDN:AAC14414.1 C;Genetics:
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A; Introns: 116/3;
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A; Accession: T51158
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Best I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGIAGAVSRTSTAPLDRLKIMMQVH----GSKSDKMNIFGGFRQMV----KEGGIRSLW
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                                                                                                                                                                                                           LPEEYRKKAQSSLLTAVLSAGIATLTC----YPLDTVRRQMQ---
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                                                                                                                                   AGIIDRDGLIGLYRGFLPNALKTLPNSSIRLTTFDMVKRLIATSEK
                                                                                                                                                                      RRIISKEGIPGLYRGITPNFMKVLPAVGISYVVYENMKQTLGVTQK
                                                                                                                                                                                                                                               WLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLEGSPQLNMVGLF
                                                                                                                                                                                                                                                                                    LRLRLAV--EPRYRTMSQVALSMLRDEGIASFYYGLGPSLVGIAPYIAVNFCIFDLVKKS
                                                                                                                                                                                                                                                                                                                     MKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYELLKSY 371
                                                                                                                                                                                                                                                                                                                                                          KGNLPQVIRVLPYSAVQLLAYESYKNLFKGKDDQLSVIGRLAAGACAGMTSTLLTYPLDV
                                                                                                                                                                                                                                                                                                                                                                                                                                   AGALAGAAAKTVTAPLDRIKLLMQTHGIRLGQQSAKKAI--GFIEAITLIAKEEGVKGYW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LREEGVASFYNGLGPSLLSIAPYIAINFCVFDLVKKSLPEKYQQKTQSSLLTAVVAAAIA
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98; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 454.5;
Pred. No. 1.
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A; Molecule type: DNA
A; Residues: 1-392 <BEV>
A; Cross-references: EMB
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R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert,
                                                                                                                                                                                                                                                                                                                                                                           adenylate translocator brittle-1 homolog F8B4.100 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr_1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
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T05350
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A;Note: F20B18.290
C;Superfamily: ADP
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A:Introns: 46/3; 75/2; 144/3; 181/1; 242/3; 284/3
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                                                                                                                         A; Introns: 181/3;
A; Note: F8B4.100
                                                                                                                                                                                                                                                                      A; Reference number: A; Accession: T05350
                                                                                                                                                                                                                                                                                                      ewes, H.W.; Mayer, K.F.X.; Schuel submitted to the Protein Sequence
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A; Residues: 1-325 <BEV>
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| SYPLALVETRNQAQAMLEGSPQLNWVGLFRRIISKEGIPGLYRGITPNFMKVLPAVGISY 462 | SYPLALVRT | 403 | Qy |
| RGLAPSLIGVVPYAATNYFAYDSLRKAYRSFSKQEKIGNIETLLIGSLAGALSSTA 31: | | 260 | DЪ |
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| KSDKMNIFGGFROMVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQY-KKLLTEEGQ 28 | | 228 | Qy |
| KKGGLTLKIKIANPS | KKGGLTLKI | 96 | DЪ |
| HSTGIDIGDSLTIPDEFTEDEKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGS 22 | HSTGIDIGD | 168 | Qу |
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Search completed: August 18, 2002, 09:23:25 Job time: 3574 sec

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Best Local Similarity
Matches 210; Conser
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16-OCT-2001
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        This
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CMC3_CAEEL
                                                                      Submitted (AUG-1995) to the EMBL/GenBank/DDBJ-!- FUNCTION: CALCIUM-DEPENDENT MITOCHONDRIAL
                                                                                                                              Eukaryota; Metazoa;
Rhabditidae; Pelodei
 between
                                                                                       McMurray A.A.;
                                                                                              STRAIN=BRISTOL N2;
                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                              Caenorhabditis elegans
                                                                                                                                                       F17E5.2
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                                                     SIMILARITY).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
                       SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS
                                       SIMILARITY: BELONGS
                                                INNER MEMBRANE (BY SIMILARITY)
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een the Swiss Ins
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                                                                                                                                                                                                                                                      ISKEGIPGLYRGITPNFMKVLPAVGISYVVYENMKQTLGV
                                                                                                                                                                                                                                                                           YETNSSEPGVLALLACGTCSSTCGQLSSYPFALVRTRLQALSITRYSPQPDTMFGQFKYI
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                                                                                                                                                                                                                                                                                                                   IKIAPETAVKFWAYEQYKKLLTEE--GQKIGTFERFISGSMAGATAQTFIYPMEVMKTRL
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45.7%;
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Ling mitochondrial carrier
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Pred. No. 1.9e:
04; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00036; efhand; 3. Pfam; PF00153; mito_carr; 3. PRINTS; PR00926; MITOCARRIER.
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InterPro; IPR002048; EF-hand.
InterPro; IPR002067; Mit_carrier
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                                                                                                                     NSTKTNKLGVVSCVHLLHAEGGIKSFWRGNGINVIKIAPESAMKFMCYDQIKRWMQEYKG
                                                                                                                                                                         DEFTEDEKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKI-
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PS00215; MITOCH_CARRIER;
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1 (POTENTIAL).
2 (POTENTIAL).
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6 (POTENTIAL).
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; Pred. No. 5e-!
91; Mismatches
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EF-HAND 4.
3 APPROXIMATE TANDEM REPE
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EF-HAND 2.
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ng as its content is in no way
road Hsage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                               137;
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RESULT
CMC1_Y
Transmembrane;
TRANSMEM 231
TRANSMEM 307
TRANSMEM 355
TRANSMEM 409
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                                         PRINTS; PROUDYS, EE_HAND; 1.

PROSITE; PSO0018; EE_HAND; 1.

PROSITE; PS00215; MITOCH_CARRIER; 1.

Hypothetical protein; Mitochondrion; Inner
Hypothetical protein; Calcium-binding.
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                                                                                                                                                                                                                           or send an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soler-Mira A., Saiz J.E., Ballesta J.P.G., Remacha M. "The sequence of a 17,933 bp segment of Saccharomyces chromosome XIV contains the RHO2, TOP2, MKT1 and END3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Las 16-OCT-2001 (Rel. 40, Las Probable calcium-binding
                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                        between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of six ORFs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Poehlmann R., Philippsen P.; "Sequencing a cosmid clone of Saccharomyces cerevisiae chromosome reveals 12 new open reading frames (ORFs) and an ancient duplicat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=S288C / FY1679;
MEDLINE=96310628; PubMed=8740422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
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                                                                                                                                                InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=S288C
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Yeast 12:485-491(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reast 12:391-402(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=S288C / FY1679;
MEDLINE=96267764; PubMed=8701611;
                                                                                                                                                                                                                                                                                                                        CAUTION: REF.1 AND REF.2 SE FRAMESHIFT IN POSITION 403.
                                                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS 4 EF-HAND CAUTION: REF.1 AND REF.2 SEQUEN
                                                                                                                                                                                                                                                                                                                                                                         inner membrane (Potential).
SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: CALCIUM-DEPENDENT MITOCHONDRIAL
                                                                                                                                                                          : Z71359; CAA95958.1;
S0005027; YNL083W.
                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                 x89016;
                                                                                                                                                                                                                        and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                              non-profit institutions as long
                                                                                                                                  IPR002048; EF-hand.
IPR002067; Mit_carrier.
IPR001993; Mitoch_carrier.
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307
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Transport;
31 248
07 326
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09 428
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Last annotation ing mitochondrial
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Q01888; 01-APR-1993 (Rel. 25, Created)
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Pred. No. 1.3e-32;
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6 (POTENTIAL).
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Grave's disease carrier protein protein homolog).
SLC25A16 OR GDA OR GDC.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; C.
Manmalia; Eutheria; Cetartiodac

protein

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(GDC) (Mitochondrial solute carrier

Mammalia; Eutheri Bovidae; Bovinae;

Cetartiodactyla;

Ruminantia;

Craniata;

Vertebrata; Euteleostomi;

Pecora;

Bovoidea;

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RESULT 5
GDC_HUMAN
ID GDC_F
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 GDC_HUMAN STAN
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SEQUENCE FROM
TISSUE=Heart;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X66035; CAA46834.1; -. PIR; S26596; S26596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fiermonte G., Runswick M.J., Walker J.E., Palmieri F.;
"Sequence and pattern of expression of a bovine homologue of a human
mitochondrial transport protein associated with Grave's disease.";
DNA Seq. 3:71-78(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
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                                                                                                                                                                                                                                                                                                                                                                                                                           inner membrane (By similarity).
TISSUE SPECIFICITY: MOSTLY IN THYROID,
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                                                                                                                                                                                                                                                                                                                                                                                         NGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIYPMEVMK 313
                                                                                                                                              LPEFEKCLTMRETMKYVYGHHGIRKGLYRGLSLNYIRCVPSQAVAFTTYELMKQ
                                                                                                                                                                               L-EGSPQLNMVGLFRRIISKEGI-PGLYRGITPNFMKVLPAVGISYVVYENMKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PR00926; MITOCARRIER.; 3. PS00215; MITOCH_CARRIER; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
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Last sequence
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Pred. No. 2.3e
54; Mismatches
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MIM; 139080;
                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
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Prohl C., Pelzer V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93091248; PubMed=1457817; Fiermonte G., Runswick M.J., Walk "Sequence and pattern of expressi mitochondrial transport protein a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90114217; PubMed=2575220;
Zarrilli R., Oates E.L., McBride O.W., Lerman M.I., Chan J.Y.,
Santisteban P., Ursini M.V., Notkins A.L., Kohn L.D.;
"Sequence and chromosomal assignment of a novel cDNA identified
immunoscreening of a thyroid expression library: similarity to
family of mitochondrial solute carrier proteins.";
Mol. Endocrinol. 3:1498-1508(1989).
                                                                                                                                Mitochondrion;
                                                                                                                                                                                      Pfam; PF00153; mito_carr;
                                                                                                                                                                                                                                                          EMBL; M31659; AAA36329.1; ALT_FRAME PIR; A40141; A40141.
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REVISIONS TO C-TERMINUS
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                                                                                                                                                                                                                      InterPro; IPR002067; Mit_
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN FROM POONWARD DUE TO A FRAMESHIFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
DISEASE: POSSIBLE ROLE IN GRAVES' DISEASE. THIS PROTEIN IS
RECOGNIZED BY IGG FROM PATIENTS WITH ACTIVE GRAVE'S DISEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Mitochondrial
                                                                                                                                                                  PR00926; MITOCARRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e G., Runswick M.J., Walker J.E., Palmie and pattern of expression of a bovine drial transport protein associated with 3:71-78(1992).
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220
332
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191
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                                                                                                                                                 MITOCH_CARRIER;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 matrix.
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123
219
                                                                        r membrane; Repeat; T
154 POTENTIAL.
211 POTENTIAL.
254 POTENTIAL.
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   36235
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solute carrier
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   CFDB8F4F3E7F0F4B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 accumulation of coenzyme A in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        accumulation
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Grave's disease
   CRC64;
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Similarity

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Length

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P16261;
01-AUG-1990
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                                                         NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-90114217; PubMed-2575220;
Zarrilli R., Oates E.L., McBride O.W., Lerman M.I., Chan J.Y.
Santisteban P., Ursini M.V., Notkins A.L., Kohn L.D.;
"Sequence and chromosomal assignment of a novel cDNA identif
immunoscreening of a thyroid expression library; similarity
family of mitochondrial solute carrier proteins.";
Mol. Endocrinol. 3:1498-1508(1989).

1- FUNCTION: NOT KNOWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
Grave'S disease carrier protein (GDC)
protein homolog) (Fragment).
SLC25A16 OR GDA.
                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS
                                                                                                              REPEAT
                                                                                                                                     REPEAT
                                                                                                                                                                                     Mitochondrion;
                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                              InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane (Potential).
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                                                                                                                                                                                                  PF00153; mito_carr; 3. TE; PS00215; MITOCH_CARRIER;
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                                                                                                                                                                                                                                                            IPR001993; Mitoch_carrier.
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123
123
3 >322
3 322
3 35056 MW;
                                                                                                                                                                                     Transmembrane;
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                                                                                                                                                                                  Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                         F78CBDA36CA9DC9A CRC64;
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(Mitochondrial solute carrier
                                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                                                                                                             Repeat
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hn L.D.;
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Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       identified
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RESULT 7
BTI_MAIZE
ID MATA
BTI_MAIZE
AC P29518;
DT 01-APR-199;
CS PERTMALE-1
GN BTI.
CC Spermatoph;
PANICOIDER
RN [1]
RN MEDLINE=93
RA NELSON O.E
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RA NELSON O.E
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CC -!- FUNCTI
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CC -!- SUBCUENCE
CC -!- TISSUENCE
CC This SWISS
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CC Use by no CC
C This SWISS
CC DETWEEN THE TOO;
DR PANISTE; PR
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FT TRANSMEM
FT TRANSMEM
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Best Local
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01-APR-1993
16-OCT-2001
                                                                                                Pfam; PF0013; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 1.
                                                                                                                                                                                                                                                                                                          use by non-profit institu modified and this statement entities requires a license
                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
                                                                                                                                                                                                     MaizeDB; 47578;
                                                                                                                                                                                                                               PIR; JQ1459; JQ1459.
                                                                                                                                                                                                                                                  EMBL; M79333;
                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   -I- FUNCTION: COULD PLAY A ROLE IN AMYLOPLAST MEMBRANE TRANSPORT
-I- SUBCELLULAR LOCATION: Chloroplast; amyloplast.
-I- TISSUE SPECIFICITY: ENDOSPERM OF DEVELOPING KERNELS.
-I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suppressor-mutator-induced m Plant Cell 3:1337-1348(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sullivan T.D., Strelow Nelson O.E. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                              InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Analysis of maize brittle-1 alleles and a Suppressor-mutator-induced mutable allele.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93005685; PubMed=1668652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays (Maize)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLKSYWLDNFA-----KDSVNPGVMVL-----LGCGALSSTCGQLASYPLALVRTRMQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVRVRLAFQVKGEHTYSGIIHAFKTIYAKEGGFLG-FYRGLMPTILGMAPYASVSFFTFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VMKTRLAVGKTGQ--YSGIYDCAKKILKHEG--LGAFYKGYVPNLLGIIPYAGIDLAVYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103;
  peptide; Chloroplast; Amyloplast; Transmembrane

1 75 CHLOROPLAST (POTENTIAL).

76 436 BRITTLE-1 PROTEIN.

M 229 247 POTENTIAL.

M 327 347 POTENTIAL.
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25, Last sequence update)
40, Last annotation update)
, chloroplast precursor.
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                                                                                                                                                                                                                                                                                     Illingworth C.A., Phillips R.L.,
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Pred. No. 5
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QS

SEQUENCE

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                013805;
15-JUL-1998
15-JUL-1998
                                                         EMBL; 298597; CAB11217.1; ... Interpro; IPR0012067; Mit_carrier. Interpro; IPR001993; Mitoch_carrier. Pfam; PF00153; mito_carr; 3.
                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                           Skelton J., Churcher C.M., Barrell B.G., Rajandream M.A., Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitoo
                                                                                                                                                                                                                                                                                                                                                                                                        Putative mitochondrial carrier C17H9.08. SPAC17H9.08.
                                                                                                                                                                                                                                                                                                     STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCHPO
TRANSMEM
           Transmembrane;
                       Hypothetical protein; Mitochondrion;
                                   PRINTS; PR00926; MITOCARRIER; PROSITE; PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomycetales; Schizosaccharomycetaceae;
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                                                                                                                                                                                                                         DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                      inner membrane (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGIDLAVYELLKSYWLDNFAK---DSVNPGVMVLLG--CGALSSTCGQLASYPLALVRTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGFASTLCTYPMELIKTRVTIEK-DVYDNVAHAFVKILRDEGPSELYRGLTPSLIGVVPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGATAQTFIYPMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGIGAFYKGYVPNLLGIIPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMQNEGWTGLFRGNAVNVLRVAPSKAIEHFTYDTAKKFLTPKGDEPPKIPIPTPLVAGAL
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Fransport.
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                                                                                                                                                                                                                                                                                                                                                                                                                          36, Created)
36, Last sequence update)
36, Last annotation updat
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34.8%;
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                         membrane; Repeat;
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or send =
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O1-JUL-1993 (Rel. 26, Createu,
O1-JUL-1993 (Rel. 26, Last sequence update,
16-CCT-2001 (Rel. 40, Last annotation update)
**no ATP carrier protein, isoform T2 (ADP/ATP
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                                                                                              the
                                                                                                                                                                                                                                                                                                                           "Two bovine genes for mitochondrial ADP/ATP translocase differences in various tissues.";
Biochemistry 28:866-873(1989).
-!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACRO
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-89229093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADT3
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Mammalia; Eutheria;
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European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed. ities requires a license agreement (See send an email to license@isb-sib.ch).
                                                                                                                                                                                      SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                DOMAIN: COMPOSED OF
                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                  SUBUNIT: HOMODIMER.
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                                                                                                                                                                                                                                      inner membrane
                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a
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Pred. No. 1.
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                          (See http://www.isb-sib.ch/announce/
                                                                 There are no rest
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                                                ons on its in no way commercial
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                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Pr
NCBI_TaxID=9606;
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P1235; 096C49;
01-OCT-1989 (Rel. 12, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
ADP/ATP carrier protein, liver isoform T2 (ADP/ATP translocase (Adenine nucleotide translocator 3) (ANT 3).
SLC25A6 OR ANT3.
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Strausberg R.;
Submitted (OCT-2001) to
                  SEQUENCE FROM N.A.
TISSUE=Cervix;
                                                       "DNA sequences of two expressed
                                                                                 SEQUENCE FROM N.A. MEDLINE=89236396; PubMed=2541251;
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                                                                         Cozens A.L., Runswick M.J.,
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                                               Mol. Biol.
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IPR001993; Mitoch_carrier.
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EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 97
                                                                                                                                                                                                                                                                          CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                  TRANSMEM
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [3]
SEQUENCE OF 3
TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Two distinct genes for ADP/ATP translocase are level in adult human liver.";
Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
-i- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long a
modified and this statement is not removed.
entitles requires a license agreement (See l
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                  Mitochondrion; Inner membrane; Multigene family.
                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                 Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 403000; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Houldsworth J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=88124845; PubMed=2829183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
             420
                                   190
                                                                               130
                                                                                                      305
                                                                                                                                                 250
                                                                                                                          70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Integral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: HOMODIMER.
                                                                                                                                                                     S03894; S03894.
B28116; B28116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inner membrane
AYFGVYDTAK-----GMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMMQSGR
                                                                                          FIYPMEVMKTRLA--VGKTG---QYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAG
                                                                                                                          FWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHTQFWRYFAGNLASGGAAGATSLC
                                                                                                                                                 LWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSM-----AGATAQT
                                                IDLAYYELLKSYWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAML
                                                                              FVYPLDFARTRLAADVGKSGTEREFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  pro; IPR002067; Mit_carr
pro; IPR001993; Mitoch_c
pr00153; mito_carr; 3.
s; PR00926; MITOCARRIER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J03592; AAA36750.1; -BC014775; AAH14775.1;
                                                                                                                                                                                                                    97;
                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Attardi
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32866
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91
134
195
195
231
291
100
208
298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mit_carrier.
Mitoch_carrier.
                                                                                                                                                                                                                                                                            ¥,
                                                                                                                                                                                                                   60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THE MITOCHONDRIAL CARRIER FAMILY
                                                                                                                                                                                                                                                                          KHTQ -> RHA (IN REF. S -> F (IN REF. 2). 18534E9F0E49672F CI
                                                                                                                                                                                                                              Score 368; DB 1;
Pred. No. 4e-17;
                                                                                                                                                                                                                                                                                                                                           1 (POTENTIAL).
2 (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
5 (POTENTIAL).
6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat;
                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAINS
                                                                                                                                                                                                                    112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein.
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                                                                                                                                                                                                                                         Length
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                                                                                                                                                                                                                                                                            CRC64;
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                                                                                                                                                                                                                    28;
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245

KGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSN---VLRGMGGAFVLVLYDELKKVI 298

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Query Match
Best Local
        Matches
                                                      TRANSMEM
TRANSMEM
TRANSMEM
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J., Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J., Kucaba T., Hillier L., Jier M., Johnston L., Langston Y., Latretlle P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L., Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEU5_YEAST
P38702;
                                                                                                                                                                                                                     use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cere
Eukaryota; Fungi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEU5
                                                                                                                        Pfam; PF00153; mito_carr;
                                                                                                                                                                                                                              the European
                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                              disease
                                                                                                                                                                                                                                                                                                                                                                                                             Science 265:2077-2082(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Vaudin M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995
16-OCT-2001
                                                                                             Mitochondrion;
                                                                                                      PROSITE;
                                                                                                                PRINTS;
                                                                                                                                  InterPro;
                                                                                                                                         SGD; S0001044; LEU5.
InterPro; IPR002067;
                                                                                                                                                                                                                                        between
                                                                                                                                                                                                                                                                                                                                     matrix.
                                                                                                                                                                                                                                                                                                                                                      "The yeast mitochondrial carrier Leu5p
                                                                                                                                                                                                                                                                                                                                                                        Prohl C., Pelzer W.,
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21106356;
                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION, AND
                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94378003; PubMed=8091229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995
                                                                                                                                                                                                                                                                  DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS. SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                       mitochondrial matrix.
                                                                                                                                                                                                                                                                                                                  FUNCTION:
                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OR YHR002W
                                                                                                                                                                                                                                                                                      inner membrane
                                                                                                                                                              S46795; S46795.
                                                                                                                                                                                                                                                                                                                           Cell. Biol.
                                                                                                                                                                      U10555; AAB68424.1;
       98;
                                                                                                                                                                                          an
                                                                                                     pr00926; MITOCARRIER.
; PS00215; MITOCH_CARRIER; 3.
                 Similarity
                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                 pean Bloinformatics Institute. The non-profit institutions as long and this statement is not removed. requires a license agreement (See
                                                                                                                                 IPR001993; Mitoch_carrier
                                                     136
208
325
357 I
                                                                                                                                                                                          email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel.
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              carrier
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356; PubMed=11158296;
zer W., Diekert K., Kmita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cerevisiae (Baker's yeast).
ngi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AB972;
                                                       AA;
                                                                                  Inner membrane; Repeat; 6 153 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                            are required
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31,
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                14.7%;
30.1%;
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                                                       ₩;
       55,
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                Score 365; DB 1; Pred. No. 7.9e-17;
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                                                       16266B2CD4B996D5
                                                                                                                                                                                                                                                                                                                 accumulation of coenzyme A in
       Mismatches
                                                                                                                                                                                                                                                                                                                                              accumulation
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                                                                                             Transmembrane;
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f
                                                                                                                                                                                                                                                                                                                                                       human homologue
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                        Length 357;
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       Indels
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                                                                                                               REVISIONS.
Laplace C.
Submitted
                                    "Expression and sequence analy translocase 1 and 2 genes."; Gene 254:57-66(2000)
                                                                        PubMed=10974536;
Levy S.E., Chen Y.-S.,
                                                                                                                                                                                                           TISSUE=Skeletal muscle; Sheldon J.G.;
                                                                                                                                                                                                                                                                              Ellison J.W.,
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                    Submitted
                                                                                                                                                              Costet P.,
                                                                                                                                                                      SEQUENCE FROM
STRAIN=129/SV;
                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                   Mamm.
                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6; TISSUE=Brain; MEDLINE=97059403; PubMed=8903
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                 SLC25A5 OR ANT2
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                                                                                             SEQUENCE
                                                                                                                                                                                           Thesis (1995),
[3]
                                                                                                                                                                                                                                                                "Rapid evolution
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                 SUBUNIT: HOMODIMER
                          MITOCHONDRIAL INNER
        SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  MOUSE
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                                                                                             FROM
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                                                                                                                                                    (FEB-1993)
                                                                                                               (FEB-1997)
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                                                                                                                                                                                N.A.
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                                                                                                                                                                                                  University
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                                                                                                                                                                                                                                                                   X., Franc
                                                                                                                                                                                                                                                                                      PubMed=8903724;
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Rodentia;
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       Integral
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P51881; 061311;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update
ADP,ATP carrier protein, fibroblast isoform
(Adenine nucleotide translocator 2) (ANT 2).
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                                                                       Juanam B.H., Waquence analysis of t 2 genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pseudoautosomal
                                                     EXCHANGE
                                                                                                                                                                                                    EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                    Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       474
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membrane
                                                                                                          Wallace D.C
of the mouse
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                                                                                                                                                                                                                                                                                                                                                                      U. K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vertebrata;
thi; Muridae;
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                            SLC25A5 OR ANT2
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EMBL; U10404; AAA19009.1; --
EMBL; X70847; CAA50196.1; --
EMBL; AF240003; AAF64471.1; --
MGD; MGI:1353496; S1c25a5.
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PF00153; mito_carr; 3.
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                                                                      (ADP/ATP
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the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@1sb-sib.ch).
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PRINTS; PR00926; MITOCARRIER;
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MEDLINE-90375457; PubMed-2168878;
Ku D.-H., Kagan J., Chen S.-T., Chang C.-
"The human fibroblast adenine nucleotide
                                                                                                                                                                                                                        PIR; C28116; C28116
MIM; 300150; -.
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Houldsworth J., Attardi G.;
"Two distinct genes for ADP/ATP translocase are
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BL; J02683; AAA35579.1; -.
BL; L78810; AAB39266.1; -.
BL; ACCO04000; AAB99347.1; -.
BL; J03591; AAA36749.1; -.
R; A29132; A29132.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        el in adult human liver.";
C. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
FUNCTION: CATALYZES THE EXCHANGE OF ADP AND
MITOCHONDRIAL INNER MEMBRANE.
SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inner membrane.
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. Chem. 265:16060-16063(1990)
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la R.A., Schl
d (JUN-1996)
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(JAN-1998)
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to the EMBL/GenBank/DDBJ
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SEQUENCE
              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                       "Isolation and characterization of cDNA clones and a genomiencoding rat mitochondrial adenine nucleotide translocator. Biochim. Biophys. Acta 1152:192-196(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94002161; PubMed=8399300;
Shinohara Y., Kamida M., Yamazaki N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, fibroblast isoform (
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                                                                                                                                                               This
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                                                                                                                                                                                                    DOMAIN: COMPOSED OF SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                SUBUNIT: HOMODIMER. SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                               MITOCHONDRIAL INNER MEMBRANE.
                                                                                                                                                                                                                                                   SKELETAL MUSCLE.
                                                                                                                                                                                                                                                                                                inner membrane.
                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RQLLAGGIAGAVSRTSTAPLDRLKIMMQV-HGSK---
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                                                                                                                                                                                                    THREE HOMOLOGOUS DOMAINS.
TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                        PRESENT IN KIDNEY,
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Sciurognathi; Muridae
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3 -> E (IN REF. 2).
R -> L (IN REF. 4 AN
V -> G (IN REF. 5).
F973C3AED92C49D3 (
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2) (ANT 2).
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N REF. 4 AND 9
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..5e-16;
nes 112;
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Matches 94
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01-MAY-1992
                                                                                                                                                                                                                        01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein, mitochondrial precursor (ADP/ATP translocase)
(Adenine nucleotide translocator) (ANT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
TRANSMEM
                                             extension.";
Curr. Genet. 20:405-410(1991).
-!- FUNCTION: CATALYZES THE EXCHANGE
                                                                               STRAIN=CV. DESIREE; TISSUE=Green MEDLINE=9224284; PubMed=1807831; Emmermann M., Braun H.P., Schnitz Emmermann M., Braun H.P., Schnitz "The ADP/ATP translocator from po
                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                           SOLTU
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REPEAT
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InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
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                                                                                                                                                                                                    Solanum tuberosum
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            SUBCELLULAR LOCATION:
                       SUBUNIT: HOMODIMER
                                   MITOCHONDRIAL INNER MEMBRANE
                                                                                                                                                                                                                                                                                              SOLTU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKRTQFWRYFAGNLASGGAAGATSLC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSM-----AGATAQT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RQLLAGGIAGAVSRTSTAPLDRLKIMMQV-HGSK---SDKM--NIFGGFRQMVKEGGIRS
                                                                                                                                                                                                                                                                                                                                                          KGTDIMYTGTLDCWRKIARDEGGKAFFKGAWSN---VLRGMGGAFVLVLYDEIKK
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94; Conservative
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           Integral
                                                                               Schmitz U.K. from potato
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 358; DB 1; 1
Pred. No. 1.8e-16;
D; Mismatches 113;
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CHAIN 78 386 ADP,AFT
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PIR; S17917; S17917.
PIR; S21974; S21974.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00926; MITOCARRIER.

PROSITE; PS00215; MITOCH_CARRIER; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitochondrion;
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                                                                                                                                                   GFNISCVGIIVYRGLYFGMYDSLKPVLLTGNLQDS----FFASFGLGWLITNGAGLASYP
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                                                                                                                                                                                                                                                                                                                                                                                                                            14.3%; Score 355.5; DB 1; Length 386; 31.2%; Pred. No. 3.6e-16; Vative 55; Mismatches 117; Indels 31; Gaps
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SPTREMBL 19:*

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sp_fungi:*

sp_fungi:*

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sp_manma!

sp_parci:*

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Gapop 10.0 , Gapext 0.5
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             sp_vertebrate:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Q9m058 arabidopsis | Q9M058 | 10 | 332 | 21.0 | 520 | 16 |
|--------------------|--------|----|--------------------------|-------|-------|--------|
| 004619 arabidopsis | 004619 | 10 | 352 | 21.0 | 521 | 14 |
| Q96usl saccharomyc | Q96US1 | ω | 545 | 24.7 | 612.5 | 13 |
| Q9he62 neurospora | Q9НЕ62 | ω | 631 | 26.3 | 652 | 12 |
| Q9fls8 arabidopsis | Q9FLS8 | 10 | 478 | 33.9 | 840 | 11 |
| Q91y28 arabidopsis | Q9LY28 | 10 | 479 | 34.3 | 852 | 10 |
| Q9fi43 arabidopsi | Q9FI43 | 10 | 487 | 35.7 | 885.5 | 9 |
| 09vtx3 drosophila | Q9VTX3 | υ | 370 | 36.4 | 902 | æ |
| Q9bsa6 homo sapien | Q9BSA6 | 4 | 311 | 44.7 | 1110 | 7 |
| Q9bv35 homo sapien | Q9BV35 | 4 | 482 | 51.8 | 1285 | 6 |
| Q96nq4 homo sapien | Q96NQ4 | 4 | 384 | 56.3 | 1397 | . UT |
| Q96pzl homo sapien | Q96PZ1 | 4 | 568 | 59.9 | 1487 | 4 |
| Q9d5g5 mus muscul | Q9D5G5 | 11 | 473 | 61.2 | 1518 | w |
| Q9p129 homo sapien | Q9P129 | 4 | 411 | 85.9 | 2132 | 2 |
| 018757 oryctolagus | 018757 | 6 | 475 | 95.6 | 2373 | 1 |
| Description | ID | DB | Query Match Length DB | Query | Score | Result |

1;

| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | ယ | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | |
|--------------------|--------|--------|--------|--------------------|--------|--------|--------|--------|--------|--------------------|--------|--------------------|--------|--------------------|--------------------|--------|--------|--------|--------|--------|--------------------|--------------------|--------|--------------------|--------|--------------------|--------|--------------------|--|
| 355.5 | 356 | 357.5 | 359 | 360 | 362.5 | 365 | 367 | 367.5 | 368 | 369 | 371 | 400.5 | 410.5 | 417.5 | 425.5 | 429.5 | 434.5 | 445.5 | 446 | 446 | 448 | 448 | 454.5 | 455.5 | 462 | 475 | 500.5 | 506 | |
| 14.3 | 14.3 | 14.4 | 14.5 | 14.5 | | 14.7 | 4. | 14.8 | | | | | | 16.8 | | 17.3 | | | 18.0 | | | | | | | 19.1 | • | 20.4 | |
| 315 | 301 | 346 | 301 | 298 | 334 | 298 | 298 | 348 | 298 | 339 | 298 | 319 | 377 | 326 | 418 | 294 | 428 | 381 | 392 | 385 | 325 | 316 | 381 | 415 | 126 | 348 | 426 | 358 | |
| 4 | ر ت | 10 | G | 13 | 10 | 4 | 13 | 10 | 13 | 10 | 13 | 10 | 5 | ω | 10 | ഗ | 10 | 10 | 10 | 10 | 10 | S | 10 | 10 | 11 | 10 | ω | 10 | |
| Q9н0С2 | Q26006 | Q9LIF7 | Q25692 | Q919M9 | Q942Z2 | Q96C49 | Q9YIC4 | Q9LJX5 | Q9PRH2 | Q9FI73 | Q9PRH1 | Q9MA27 | Q9VDL7 | Q12251 | Q9C9R4 | Q93717 | Q9LV81 | Q9LD54 | Q9SUV1 | Q9ZNY4 | Q9SZI9 | Q9NI37 | 065023 | Q9M024 | Q99KD3 | Q9SH98 | 094502 | Q9M333 | |
| Q9h0c2 homo sapien | 7 | 7 | ~ | Q9i9m9 xenopus lae | N | ₽ | | | | Q9fi73 arabidopsis | | Q9ma27 arabidopsis | | Q12251 saccharomyc | Q9c9r4 arabidopsis | C | | | | | Q9szi9 arabidopsis | Q9ni37 trichomonas | | Q9m024 arabidopsis | | Q9sh98 arabidopsis | ທ | Q9m333 arabidopsis | |

ALIGNMENTS

| Qu Be Ma | RRS7517 ID 87517 ID 8 |
|--|--|
| Query Match Best Local Simi Matches 454; | O18757 O18757 O18757 O18757 O18757 O1-JAN-1998 (TIEMBL O1-JAN-1998 (TIEMBL O1-JAN-1998 (TIEMBL O1-DEC-2001 (TIEMBL DECOXISOMAL CA-DEPE OVYCTOLAGUS CHORICUL EUKARYOTA; MCTAZOA; MAMMALIA; EUTHORIA; ICHTAXID-9986; [1] SEQUENCE FROM NA. MEDLINE-97385133; P Weber F.E., Minestr Compassi S., Wehrli "Molecular cloning mitochondrial carri "Molecular cloning mitochondrial carri "FOO. Natl. Acad. S1 - SIMILARITY: TO EMBL; AF004161; AAB HSSP; P09860; 3CTN. InterPro; IPR002048 InterPro; IPR002048 InterPro; IPR002048 InterPro; IPR002048 InterPro; IPR002067 Pfam; PF00153; mito PRINTS; PR00926; MT SMART; SM00054; Efha Pfam; PF00153; mito PRINTS; PR00926; MT SMART; SM00054; Efha PFAM; PS00018; E Calcium-binding. ECALCIUM-binding. |
| h Similarity 95.2%; 54; Conservative | MMBLz MMBLz MMBLz MMBLz ia; ia; ia; ia; ia; ia; ia; ia; ia; ia |
| %; Score 2373; %; Pred. No. 3.7 | ARY; PRT; 475 AA. el. 05, Created) el. 05, Last sequence update) el. 19, Last annotation update) DENT SOLUTE CARRIER. Chordata; Craniata; Vertebrata; Eut Lagomorpha; Leporidae; Oryctolagus. bMed=9238007; Lagomorpha; Leporidae; Oryctolagus. bMed=9238007; Lagomorpha; Leporidae; Oryctolagus. bMed=9238007; Lagomorpha; Leporidae; Oryctolagus. bMed=9238007; Lagomorpha; Leporidae; Oryctolagus. Lagomorpha; Leporidae; Oryctolagus. bMed=9238007; Lagomorpha; Leporidae; Oryctolagus. Lagomorpha; Leporidae; Oryctolagus. bMed=9238007; Lagomorpha; Leporidae; Oryctolagus. bMed=9238007; Lagomorpha; Leporidae; Oryctolagus. bMed=9238007; Lagomorpha; Leporidae; Oryctolagus. bMed=9238007; Lagomorpha; Leporidae; Oryctolagus. bMit_carrier. d, 4. Lagomorpha; Leporidae; Oryctolagus. bMit_carrier. d, 4. Lagomorpha; Leporidae; Oryctolagus. carr; 3. |
| ; DB 6; 3.7e-170; hes 9; | Created) Last sequence update) Last sequence update) Luff CarRIER. it). a; Craniata; Vertebrata; pha; Leporidae; Oryctola 38007; Dyer J.H., Werder M., Bomas R.M., Schulthess G., coxisomal Ca2+-dependent family."; A. 94:8509-8514(1997). A. 94:8509-8514(1997). A. 94:8509-8514(1997). A. Garrier d. dcarrier. rrier. R. UNKNOWN_3. |
| Length 475; Indels 2; | ata; Euteleostomi; colagus. Boffelli D., G., Hauser H.; ent member of the |
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01-OCT-2000 (TrEMBLrel. 15, C
01-OCT-2000 (TrEMBLrel. 15, L
01-DEC-2001 (TrEMBLrel. 19, L
CALCIUM BINDING TRANSPORTER (
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InterPro; IPR001093; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 2.
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                                                                                                                                                                                                                                                             PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning and subcellular localization transporter.";
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLAVYELLKSYWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLE 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGA
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TAQTFIYPMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISEQQAELILQSIDADGTMTVDWNEWRDYFLFNPVADIEEIIRFWKHSTGIDIGDSLTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISEQQAELILQSIDVDGTMTVDWNEWRDYFLFNPVTDIEEIIRFWKHSTGIDIGDSLTI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAQTFIYPMEVMKTRLAVGKTGQYSGIYDCAKKILKYEGFGAFYKGYVPNLLGIIPYAGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B., Valle D.;
                                                                                                                      Similarity
                                                                                                                                                                                                                                                             PS00018;
                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N.A.
                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                          EF_HAND; UNKNOWN_3
                                                                                                                                                                                                                 45819
                                                                                                                   99
                                                                                                                   . 88;
                                                                                                                                                                                                                 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ
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Last annotation updat
(FRAGMENT).
                                                                                         Score 2132; Depred. No. 4e-10; Mismatches
                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                 99A3B5BAD9C2A4CF CRC64;
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                                                                                                                   4e-152;
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                                                                                           Gaps
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9D5G5 PRELIMINARY;
Q9D5G5;
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-DEC-2001 (TREMBLREL. 1
PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=C57BL/6J; TMEDLINE=21085660;
                                                                                                                  HSSP; 064537; 1DVI.
MGD; MGI:1921936; 4930443G12Rik.
InterPro; IPR0002048; EF-hand.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4930443G12RIK
                                                         PRINTS; PR00926; MITOCARRIER. SMART; SM00054; EFh; 4.
                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                   Wynshaw-Boris A.,
Hayashizaki Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQMVKEGGI
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PS00018; I
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6J; TISSUE=TESTIS;
5660; PubMed=11217851;
Shibata K.
   ; EF_HAND;
A; 53375 1
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17,
19,
   ME.
UNKNOWN_1.
MW; 6EF920A84651EE63
                                                                                                                                                                                                                                                                                                                                                                   full-length
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                          mouse
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                                                                                                                                                                                                                                                                                                                                                                       collection.";
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
KIAA1896 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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HOmo sapiens (Human).
Homo sapiens (Human).
'harvota; Metazoa; Chordata;
'harvia; Primates;
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"Prediction of the coding sequences
The complete sequences of 60 new cDl
large proteins.":
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es. 8:179-187(2001).
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87; Mismatches
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No. 2
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NA clones from brain
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2.1e-103;
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                                                                                                                                                                                                                                                                                                                                                     096NQ4;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ30339 FIS, CLONE BRACE2007401, MODERATELY SIMILAR
                                                                                                                                             "NEDO human cDNA sequencing project."; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ EMBL; AK054901; BAB70825.1; -.
                                                                                                                                                                                                                                                                                          Homo sapiens (Human),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Euthoria; Primates; Catarrhini; Hominidae;
NCBI_TaxID-9606;
                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                               TISSUE=CEREBELLUM;
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Pred. No. 6.8e-97;
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Q1-JUN-2001 (TrEMBLrel. 17, La
Q1-DEC-2001 (TrEMBLrel. 19, La
HYPOTHETICAL 54.0 KDA PROTEIN.
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Strausberg R.;
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SEQUENCE 482 AA; 54035 MW;
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InterPro; IPR001993; Mitoch_carrier.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9BV35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                171
                                                                                                                                                                           124
244
                                                                                                                                                                                                                    133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242
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                                          206
                                                                                     184
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Local Similarity
nes 242; Conserv
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                                                                                                                                                                                                                                                                                                                                                                          DAEQPTRYETLFQALDRNGDGVVDIGELQEGLRNLGIPLGQD----AEEKIFTTGDVNKD
                                                                                 TVLARRSGSHLKSQHFGRPKWADHEVLDIGECLTVPDEFSKQEKLTGMWWKQLVAGAVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVSRTGTAPLDRLKVFMQVHASKTNRLNILGGLRSMVLEGGIRSLWRGNGINVLKIAPES
                                        AVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQMVKEGGIRSLWRGNGTNVIKIAPET
                                                                                                                                                                           SMDRDGTMTIDWQEWRDHFLLHSLENVEDVLYFWKHSTLSSAGFSAWIKDSTAEQNRSKT
                                                                                                                                                                                              SIDVDGTMTVDWNEWRDYFLFNPVTDIEEIIRFWKHST
                                                                                                                                                                                                                                                             GGLDLEEFSRYLQEREQRLLLMFHSLDRNQDGHIDVSETQQSFRALGISISLEQAEKILH
                                                                                                                                                                                                                                                                                                      GKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQAELILQ 132
                                                                                                                                                                                                                                                                                                                                                   DAERRQRWGRLFEELDSNKDGRVDVHELRQGLARLG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPAVSISYVVYENMKQALGVTSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPAVGISYVVYENMKQTLGVTQK 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSTCGQIASYPLALVRTRMQAQASIEGGPQLSMLGLLRHILSQEGMRGLYRGIAPNFMKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSTCGQLASYPLALVRTRMQAQAMLEGSPQLNMVGLFRRIISKEGIPGLYRGITPNFMKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pro; IPR002067; Mit_carrier
PF00153; mito_carr; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tted (JAN-2001) to the EMBL/GenBank/DDBJ BC001656; AAH01656.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00018; EF_HAND; UNKNOWN_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RETINOBLASTOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1285;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8917BEA2BC2FE42B
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         482
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
.6e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DВ
                                                                                                                                                                                                                                                                                                                                                 -GGNPDPGAQQGISSEGDADPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                                                                                                                                         78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  482;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                            205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301
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                                        265
                                                                                                                                                                           183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361
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  303
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Q PRESULT
D PRES
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  B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 203
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01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JDC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 34.0 KDA PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-2001) to the EMBL/GenBank/DDBJ EMBL; BC005163; AAH05163.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9BSA6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001993; Mitoch_carrier
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=MUSCLE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
  307
                                                473
                                                                                                 247
                                                                                                                                               413
                                                                                                                                                                                                  187
                                                                                                                                                                                                                                              353
                                                                                                                                                                                                                                                                                               127
                                                                                                                                                                                                                                                                                                                                               293
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                                                                                                                                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIIPYAGIDLAVYELLKSYWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTR 412
                                                                                                                                                                                                                                                                                                                        ISGSMAGATAQTFIYPMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLL::||:|| || || : || || || :|| :||
                                                                                                                                                                                                                                                                                                                                                                                             GIVGGFTQMIREGGARSLWRGNGINVLKIAPESAIKFWAYEQIKRLVGSDQETLRIHERL 126
                                                                                                                                                                                                                                                                                                                                                                                                                       NIFGGFROMVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MVLLGCGALSSTCGQLASYPLALVRTRMQAQ
GVQSR
                                              GVTQK 477
                                                                                                 MQAQAMLEGSPQLNMVGLFRRIISKEGIPGLYRGITPNFMKVLPAVGISYVVYENMKQTL
                                                                                                                                                                                                  GIIPYAGIDLAVYETLKNAWLQHYAVNSADPGVFVLLACGTMSSTCGQLASYPLALVRTR
                                                                                                                                                                                                                                                                                               VAGSLAGAIAQSSIYPMEVLKTRMALRKTGQYSGMLDCARRILAREGVAAFYKGYVPNML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVLLACGTISSTCGQIASYPLALVRTRMQAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYELLKSYWLDNFAKDSVNPGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVKFWAYEQYKKLLTEEGQKIGTFEREISGSMAGATAQTFIYPMEVMKTRLAVGKTGQYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLLDCARRILEREGPRAFYRGYLPNVLGIIPYAGIDLAVYETLKNWWLQQYSHDSADPGI
     311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RHABDOMYOSARCOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1110; DB 4;
Pred. No. 1.9e-75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNKNOWN_2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                               352
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RESULT Q9VTX3

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                                                                                                                                RA Addams D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams D., Celniker S.E., Hilbrids S., Ashburner M., Henderson S.N.,
RA Burandon R.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burton R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Buril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
RA Borkova D., Botchan M.R., Bouck J., Borkstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Clerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Clerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Closek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Goldek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegvam C.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Harris N.L., Malush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Harris N.L., Welson K.A., Howland T.J., Wei M.-H., Ibegvam C.,
RA Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Nelson D.L.,
RA Reinert K., Remington K.S., Sunders R.D.C., Scheeler F., Shen H.,
RA Sylers E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Sylers R., Weissarman D.A., Weinstock G.M., Weissenbach J.,
RA Weisson K.A., Woodaye T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Harris R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Ra Harris R., Fercior G., Turner R., Venter E., Wang A.H., Wang X.,
Ra Harris R., Fercior G., Turner R., Venter E., Wang A.H., Wang X.,
Ra Harris R., Fercior G.,
                                        Query Match
Best Local S
Matches 182
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Q9VTX3;
01-MAY-2000
01-MAY-2000
01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
Pterygota;
                                                                                                                                SEQUENCE 370
                                                                                                                                                                Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 1.
                                                                                                                                                                                                                    FlyBase; FBgn0036283; CG4392.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
                                                                                                                                                                                                                                                                       -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).
-I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
EMBL; AE003541; AAF49922.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20196006; PubMed=10731132;
       159
IEEIIRFWKHSTG--IDIGDSLTIPDEFTEDEKKSGQWWRQLLAGGIAGAVSRTSTAPLD 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN.
                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neoptera; Endopte
a; Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                AA; 41539 MW;
                                                       36.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endopterygota; Diptera; ilidae; Drosophila.
                                      58;
                                  Score 902; DB
Pred. No. 1.1e
58; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation updat
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                                                                                                                              Transmembrane; Ti
9A4F1BA9A9E5CCE1
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                            DB 5;
1.1e-59;
75;
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                                                                                                                            Transport.
El CRC64;
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Q9FI43
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                                                                                                                                                                                                                                                                                                   Matches
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Best Local Similarity
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01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
CALCIUM-BINDING TRANSPORTER-LIKE PROTEIN.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002048; EF-hand.
InterPro; IPR001993; Mitcch_carri
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; Mitc_carr; 3.
PRINTS; PR00926; MITOCARRIER.
SMART; SM00054; EFh; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P1 and TAC clones.";
DNA Res. 6:183-195(1999).
EMBL; AB017063; BAB08751.1;
HSSP; P09860; 1FI5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., K
Miyajima N., Tabata S.;
"Structural analysis of Arabidopsis thaliana chromosome
Sequence features of the regions of 1,011,550 bp covered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=COLUMBIA; PubMed=10470850; MEDLINE=99397451; PubMed=10470850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00018; EF_HAND; UNKNOWN_1
SEQUENCE 487 AA; 54505 MW; 2268B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3702;
                              139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       434
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EQPTRYETLFQALDRNGDGVVDIGELQEGLRNLGIPLGQDAEEKIFTTGDVNKDGKLDFE
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                                                                                 EFRRYMDDKELELYRIFQAIDVEHNGCISPEGLWDSLVKAGIEIKDEELARFVEHVDKDN
                                                                                                                             EFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQAELILQSIDVDG
                                                                                                                                                                                        ERDLRIRSLFSFFDSENVGYLDCAQIEKGLCALQIPSGYKYAKELFRVCDANRDGRVDYH
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                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                      35.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mitoch_carrier.
                                                                                                                                                                                                                                                                                                ; 68
                                                                                                                                                                                                                                                                                                                         Score 885.5; DB 1
Pred. No. 2.9e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                   2268B650C8841537 CRC64;
                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                             Indels
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Best Loc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000
01-OCT-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                     Pfam; PF00153; mito_carr; 3.

PRINTS; PR00926; MITOCARRIER.

SMART; SMO0054; EFh; EF-HAND; UNKNOWN_2.

PROSITE; PS00018; EPSP_SYNTHASE_1; UNKNOWN_1.

PROSITE; PS00104; EPSP_SYNTHASE_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bevan
Rudd S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002048; EF-hand.
InterPro; IPR001986; EFSP_syntase.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR002067; Mit_carrier.
IPR00153; Mito_carr; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnollophyta; Eudiotytedons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY EMBL; AL163912; CAB87921.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EU Arabidopsis sequencing project; Submitted (APR-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                    Local :
          79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INNER MEMBRANE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s.
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     EFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQAELILQSIDVDG
                                                                                                      EQPTRYETLFQALDRNGDGVVDIGELQEGLRNLGIPLGQDAEEKIFTTGDVNKDGKLDFE
                                                                                                                                                            181;
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                                                        EREIRIRSLFDFFDNSNLGFLDYAQIEKGLASLQIPPEYKYARDLFRVCDANRDGRVDYQ
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M., Murphy G., Ridley P., H
S., Lemcke K., Mayer K.F.X.;
                                                                                                                                                                                                                                                                                        membrane; Mitochondrion; NCE 479 AA; 53969 MW;
                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (APR-2000)
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
CA-DEPENDENT SOLUTE CARRIER-LIKE PROTEIN
                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N.A.
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                                                                                                                                                         90;
                                                                                                                                                         Score 852; DB Pred. No. 9.3e-90; Mismatches
                                                                                                                                                                                                                                                                                        Transmembrane; Transport. 38D58E1395316D6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hudson
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                                                                                                                                                         DB 10;
).3e-56;
les 172;
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                                                                                                                                                                                                          Length
                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eudicots; Rosid
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                                                                                                                                                         16;
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                                                                                                                                                         6;
PRESULT
OFFISE
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                                                                                                                                                                                                                                               ramada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M.
Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G.
Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
Ishida J., Jones T., Kamiya A., Karlin Neumann G., Kawai J., Kim (
Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M.,
Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,
Theologis A.;
"Fill Toract"
                                                                                                                                                      Submitted (SEP-2001) to the EMBL/GenBank/DDBJ EMBL; AB010069; BAB10081.1; -. EMBL; AY056219; AAL07068.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Structural analysis of Arabidopsis thaliana c Sequence features of the regions of 1,456,315 physically assigned Pl and TAC clones."; DNA Res. 5:41-54(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=COLUMNIA PU
MEDLINE=98290546; Pu
Kaneko T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                   InterPro; IPR002048; EF-hand.
InterPro; IPR001093; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; mito_carr; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tabata
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                          PRINTS;
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                                                                                                                                                                                                                                  "Full Length cDNA of
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KGEGLRGFYRGLLPNLLKVVPAASITYIVYEAMKKNMAL
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SEQUENCE
                                                                                                                                     German Neurospora genome project;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AL451012; CAC18152.2; -
                                                                                                                                                                                                                    Schulte U., Aign V., Hoheisel J., Brandt P., Nyakatura G., Mewes H.W., Mannhaupt G.; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                            Neurospora crassa.
Eukaryota; Fungi; Ascomycot
Sordariales; Sordariaceae;
NCBI_TaxID=5141;
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01-MAR-2001 (TIEMBLIEL 16, Created)
01-DEC-2001 (TIEMBLIEL 19, Last sequence update)
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RELATED TO PEROXISOMAL CA-DEPENDENT SOLUTE CARRIER
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                                                Score 652; DB
Pred. No. 1.6e
99; Mismatches
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Pred. No. 7.4e-55;
8; Mismatches 171;
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No. 1.6e-40;
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Belenkiy R., Wohlrab H.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ
EMBL; AF419344; AAL26493.1; -.
SEQUENCE 545 AA; 61270 MW; 8F33AA9AE392538
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                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidieursids II; Brassicales; Brassicaceae; Arabidopsis.
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01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 19, Last samotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
PUTATIVE CARRIER PROTEIN (AT4G01100/F2N1_16)
A_IG002N01.16 OR AT4G01100.
Lamar B., Stoneking Mayer K.F.X.; Submitted (MAR-2000)
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  EMBL/GenBank/DDBJ
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6; Mismatches 190;
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EMBL; AF007259; AAB61037.1; -.
EMBL; AF161491; CAB80919.1; -.
EMBL; AF360168; AAK25878.1; -.
EMBL; AF360188; AAK25878.1; -.
EMBL; AF412085; AAL07192.1; -.
EMBL; AF412085; AAL06538.1; -.
InterPro; IPR001993; Mitoch_carrier.
InterPro; IPR002067; Mit_carrier.
Pfam; PF00153; Mito_carr; 3.
PRINTS; PR00926; MITOCARRIER; UNKN
SEQUENCE 352 AA; 38325 MW; 360CA47
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SEQUENCE FROM N.A.
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Submitted (MAR-2000
[5]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M. Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bow Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., J. Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted [7]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim (Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
"Full Length cDNA of gene AT4g01100 (GI:7267607).";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Theologis A.;
"Full Length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Arabidopsis cDNA clones.";
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Yu S., Bowser
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                                                                                                                                                                                                                                                                                    Local Similarity
nes 115; Conserv
                                                                                                                                                                         RQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMN-IFGGFRQMVKEGGIRSLWRGN
                                                                                         YPMDMVRGRLTVQTANSPYQYRGIAHALATVLREEGPRALYRGWLPSVIGVVPYVGLNFS
                                                                                                          YPMEVMKTRLAVGKTG---QYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLA
                                                                                                                                                         GTNCARIVPNSAVKFFSYEQASNGILYMYRQRTGNENAQLTPLLRLGAGATAGIIAMSAT
                                                                                                                                                                                                                       KSLFAGGVAGGVSRTAVAPLERMKILLQVQNPHNIKYSGTVQGLKHIWRTEGLRGLFKGN
                                  VYESTKD
                                                              VYELLKSYWLDNFAKDSVNP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          opsis sequencing project; (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MAR-2001)
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Quach H.L., Tang C., Toriumi
L., Carninci P., Chen H., Con
L., Carninci P., Chen H., Con
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                                NPYGLVENNELTVVTRLTCGAIAGTVGQTIAYPLDVIRRRMQ
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he EMBL/GenBank/DDBJ datab
                                                                                                                                                                                                                                                                                     64;
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   LNMVGLFRRIISKEGIPGLYRGITPNFMKVLPAVGIS
                                                                                                                                                                                                                                                                                  Score 521; DB 10;
Pred. No. 4.6e-31;
4; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                 ER; UNKNOWN_1.
360CA4785EFB4A8B
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                                                    -GVMVLLGCGALSSTCGQLASYPLALVRTRMQ
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                                                                                                                                                                                                                                                                                     94;
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Bowser L.,
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n J.,
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Ecker J.R.,
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C STRAIN-CV NIPPONBARE;

A Sasaki T., Matsumoto T., Yamamoto K.;

A Correspondence T., Yamamoto K.;

T Clone:P0024G09.",

Clone:P0024G09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 117; Conserv
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
"""*SIMOTO T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR 2001 (TrEMBLrel. 16, Created)
01-MAR 2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TREMBLREL 17, Last annotation update)
01-JUN-2001 (TREMBLREL 17, Last annotation update)
01-JUN-2001 (TREMBLREL 17, Last annotation update)
07-JUN-2001 (TREMBLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sasak1 T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
clone:P0019D06.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9FU82
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GNGTNVIKIAPETAVKFWAYEQYKKL-----LTEEGQKIGTFERFISGSMAGATAQTFI 306
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                                                                                                                                                                              ESLRSHWQMERPQDS--PAVVSLFS-GSLSGIASSTATFPLDLVKRRMQLQGAAGTSSVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 520; DB 10;
Pred. No. 4.7e-31;
1; Mismatches 103;
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Search completed: August 18, 2002, 09:30:28 Job time: 483 sec

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Database
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Maximum DB seq length: 2000000000
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Perfect score:
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(ggn2_6/ptodata/1/pna/PCTUS_COMB.seq:*

(cgn2_6/ptodata/1/pna/US06_COMB.seq:*

(cgn2_6/ptodata/1/pna/US080_COMB.seq:*

(cgn2_6/ptodata/1/pna/US080_COMB.seq:*
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Listing first 45 summaries
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'Cgn2_6/ptodata/1/pna/US092_COMB.seq:*
'Cgn2_6/ptodata/1/pna/US093_COMB.seq:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 3322224 332224 332224 332224 332224 | Result No. |
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| 100 900 900 900 900 900 900 900 900 900 | ry ch |
| 3545 3545 3545 3545 3545 3545 3545 3545 | Length |
| 3121131 20 20 20 20 20 20 20 20 20 20 20 20 20 | ₽B |
| US-09-777-921-1 US-09-652-121-6793 US-09-652-121-669 US-09-652-121-669 US-09-652-121-1669 US-09-652-113-9069 US-09-652-113-1669 US-09-652-113-1669 US-09-652-113-300-3002 US-09-710-285-1759 US-09-726-8110-3387 US-09-726-8110-3387 US-60-217-3610-23662 US-60-172-360-23662 US-60-218-561-2850 PCT-US01-04098A-755 PCT-US01-04098A-755 PCT-US01-14827-2497 US-09-644-869-8718 US-09-644-869-8718 US-09-652-127-8091 US-09-677-921-3 US-09-777-921-3 US-09-777-921-3 US-09-779-921-3 US-09-785-301-54 US-09-359-922-4478 US-09-359-922-4478 US-09-359-922-4478 US-09-359-922-4478 US-09-359-922-4478 US-09-359-922-4478 US-09-359-922-4478 US-09-359-922-4478 US-09-359-118-1544 | ID |
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RESULT 1
US-09-777-921-1
Sequence 1, Application US/09777921
GENERAL INFORMATION:
APPLICANT: MERKULOV et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORT
TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001103
CURRENT FILING DATE: 2001-07-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2673
TYPE: DNA
ORGANISM: Human
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Sequence 60, Appl
Sequence 410, App
Sequence 410, App
Sequence 60, Appl
Sequence 60, Appl
Sequence 95, Appl
Sequence 95, Appl
Sequence 739, App
Sequence 741, App
Sequence 741, App
Sequence 739, App
Sequence 731, App
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RESULT 2
US-09-522-303-1193
Sequence 1193, Application US/09522303
Sequence 1193, Application US/09522303
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Gearing, Douglas A.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES DEF
TITLE OF INVENTION: HUMAN MAMMARY EPITHELIUM I
FILE REFERENCE: 1600.1086-00.01
CURRENT APPLICATION NUMBER: US/09/522,303
CURRENT FILING DATE: 2000-03-08
EARLIER APPLICATION NUMBER: 60/123,393
EARLIER FILING DATE: 1999-03-08
VUMBER OF SEO ID NOS: 1353
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1193
LENGTH: 3537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LENGTH: 3537
; TYPE: DNA
; ORGANISM: HOMO:
US-09-522-303-1193
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RESULT
US-09-649-163-8441
US-09-649-163-8441
Sequence 8441, Application US/09649163
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Helby, Kevin R.
APPLICANT: Leiby, Kevin R.
APPLICANT: Wingsbury, Gillian A.
APPLICANT: Weich, Nadine S.
APPLICANT: WeCarthy, Sean A.
APPLICANT: Milliamson, Mark
APPLICANT: Richardson, Jennifer
APPLICANT: MacBeth, Kyle J.
APPLICANT: WacBeth, Kyle J.
APPLICANT: Villeval, Jean-Luc M.G.

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; ORGANISM: Homo sapiens
US-09-649-163-8441
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SOFTWARE: Fast
SEQ ID NO 8441
FRIGTH: 3545
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Best Local Similarity
Matches 2549; Conserv
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CURRENT FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: 60/150,608
PRIOR FILING DATE: 1999-08-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1164-001
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                       ctgttacagacattgaggaaattatccgtttctggaaacattctacaggaattgacatag
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Silos-Santiago, Inmaculada
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Pred. No. 0;
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| 1800 | cagaaatgttcaaaatcatagttttaatgtgttttgaaaaggccacacaattatacttta : | 74 | Qy |
|------|--|------|----|
| 1785 | acaaaagggaagatggtaacaatggtcacttcaaacttttgggctaaattatatgtaca | 1726 | Дb |
| 7 | ggaagacggtaacaatggtcacttcaaactttttgggctaaattatatgtaca | 89 | Ωу |
| 1725 | ggagtgactttttctcctcgaattgaaacaagtctatggcaaaagaagctgcatttttt | 1666 | Db |
| 1680 | ggagtgactttttctccctcgaattgaaacaagtctatggcaaaagaagctgcattttttt | 1621 | Qy |
| 1665 | ccagaaatgatgttgcattttttgctttagcctgataattgaaactttcaacaatctct | 1606 | Db |
| Ġ | cccagaaatgatgttgcattttttgctttagcctgataattgaaactttcaacaatctct | 1561 | Qу |
| 1605 | | 1546 | Дb |
| UT. | tccctgctgtaggcatcagttatgtggtttatgaaaatatgaagcaaactttaggagtaa | 1501 | Qy |
| Ċπ | | 1486 | Db |
| 1500 | tttccaaagaaggaataccaggactttacagaggcatcaccccaaacttcatgaaggtgc | 1441 | Qy |
| 1485 | ctcaagccatgttagaaggttccccacagctgaatatggttggcctctttcgacgaatta | 1426 | Db |
| 1440 | ctcaagccatgttagaaggttcccccacagctgaatatggttggcctctttcgacgaatta | 1381 | Qy |
| 1425 | ccagcacctgtggtcagctggccagctacccattggctttggtgagaactcgcatgcagg | 1366 | Db |
| 1380 | ccagcacctgtggtcagctggccagctacccattggctttggtgagaactcgcatgcagg | 1321 | Qу |
| 1365 | attttgcaaaagattotgtaaaccotggagtcatggtgttgctgggatgcggtgccttat | 1306 | ДЪ |
| 1320 | attttgcaaaagattctgtaaaccctggagtcatggtgttgctgggatgcggtgccttat | 1261 | Ωу |
| 1305 | taccttatgcaggcatagatcttgctgtgtatgagctcttgaagtcctattggctggata | 1246 | Db |
| 1260 | taccttatgcaggcatagatcttgctgtgtatgagctcttgaagtcctattggctggata | 1201 | Qy |
| 1245 | tgaaacatgaaggcttgggagctttttacaaaggctatgttcccaatttattaggtatca | 1186 | DЬ |
| 1200 | tgaaacatgaaggcttgggagctttttacaaaggctatgttcccaatttattaggtatca | 1141 | Qy |
| 1185 | ggctggctgtaggcaaaactgggcagtactctggaatatatgattgtgccaagaagattt | 1126 | Db |
| 1140 | ggctggctgtaggcaaaactgggcagtactctggaatatatgattgtgccaagaagattt | 1081 | Qy |
| 1125 | gttccatggctggagcaactgcacagacttttatatatccaatggaggttatgaaaacca | 1066 | Db |
| 0 | gttccatggctggagcaactgcacagacttttatatatccaatggaggttatgaaaacca | 1021 | Qy |
| 1065 | acaagaagttacttactgaagaaggacaaaaaaataggaacatttgagagatttattt | 1006 | Db |
| 0 | acaagaagttacttactgaagaaggacaaaaaataggaacatttgagagatttattt | 961 | Qy |
| 1005 | gtacaaacgtcatcaaaattgctcctgagacagctgttaaattctgggcatatgaacagt | 946 | DЬ |
| | gtacaaacgtcatcaaaattgctcctgagacagctgttaaattctgggcatatgaacagt | 901 | Qy |
| 945 | ttggtggctttcgacagatggtaaaagaaggaggtatccgctcgct | 886 | Db |
| 0 | ttggtggctttcgacagatggtaaaagaaggaggtaatccgcttcgctttggaggggaaatg | 841 | Qy |
| 885 | tygaccgtctgaaaatcatgatycaggttcacggttcaaaatcagacaaaatgaacatat | 826 | Db |
| 4 | tggaccgtctgaaaatcatgatgcaggttcacggttcaaaatcagacaaaatgaacatat | 781 | Qy |
| 825 | ggaggcagcttttggcaggaggcattgctggtgctgtctctcgaacaagcactgcccctt | 766 | Db |
| œ | ggaggcagcttttggcaggaggcattgctggtgctgtctctcgaacaagcactgcccctt | 721 | Qy |
| 765 | aatggt | 706 | Db |

US-09-652-121-6793

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RESULT 4
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PRIOR FILING DATE: 1999-08:
NUMBER OF SEQ ID NOS: 7615
SOFTWARE: FastSEQ for Windc
SEQ ID NO 6793
LENGTH: 3545
                                                           APPLICANT: Distefano, Peter TITLE OF INVENTION: NOVEL NUCLE TITLE OF INVENTION: THEREFOR FILE REFERENCE: 1600.1188-001 CURRENT APPLICATION NUMBER: US/O CURRENT FILING DATE: 2000-08-30
TYPE: DNA ORGANISM:
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US-09-008
Sequence 9069, APP-1
Sequence 9069, APP-1
SERRAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MO
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1186-001
CURRENT APPLICATION NUMBER: US/09/652,12?
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,135
PRIOR APPLICATION NUMBER: 60/151,135
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 9796
NUMBER OF SEQ ID NOS: 9796
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| 261 attitgcaaaagattctgtaaaccctggagtcatggtgttgctggggatgcggtgccttat 132 | | 20 | ccttatgcaggcatagatcttgctgtgtatgagctcttgaagtcctattggctggata | 26 30 |
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| 2445 | tgcagagcatctttgttttcctttgtcctttgtttcctaccttttgaatcagattccgt | 2386 | Db |
|------|---|----------|------|
| 2400 | ctgcagagcatctttgttttcctttgtcctttgtttcctaccttttgaatcagattccgt | | Qy |
| 2385 | ttatcctgccattgctttgaaaagcagcaggaaacgaaatcctttgacttgtatcagctt | 2326 | Db |
| 2340 | tatcctgccattgctttgaaaagcagcaggaaacgaaattttttgacttgtatcagctt | 2281 | Qy |
| 2325 | aattttcagtatattactgttaaattaccaacacaaggcaatttattt | 2266 | Db |
| 2280 | attttcagtatattactgttaaattaccaacaaggcaatttattt | 2221 | Qy |
| 2265 | 4- | N | Db |
| 2220 | cagtgggcacttttccattttaccactgtaccattatttggttcctggagttatacact | 2161 | Qy |
| 2205 | tgaatacgaatgaacacagtggtggaatttctgaagggaagtgatgaaattatatttatt | 2146 | Db |
| 2160 | gaatacgaatgaacacagtggtggaatttctgaagggaagtgatgaaattatatttatt | \vdash | Qу |
| 2145 | taccttacagcaaaagcatccaaataagtatagggtttatgtccttatttttctttc | | Db |
| 2100 | accttacagcaaaagcatccaaataagtatagggtttatgtccttatttttctttc | 0 | Qy |
| 2085 | tatagatttotttaaatttoottatagaaocattaatagaaatoattacatttaaaata | 0 | рb |
| 2040 | atagatttctttaaatttccttatagaaccattaatagaaaatcattacatttaaaata | 98 | Qy |
| 2025 | ttacgtttatgccagttcctttatatttaaatttcttgttttatatattttgaatgtctt | | Db |
| 1980 | tacgtttatgccagttcctttatatttaaatttcttgttttatatattttgaatgtct | 9 | Qy |
| 1965 | ttgaacaaaatttgttttgtgtgttagagttataaatcattaatctttatttcgggtgt | | Db |
| | tgaacaaaatttgttttgtgtgttagagttataaatcattaatctttatttcgggtggt | œ | Qy |
| 1905 | tottttottaataatootgoaaatototgoootgaatoogaaatotgaaaatgtactggo | 8 | Db |
| 1860 | cttttcttaataatcctgcaaatctctgccctgaatccgaaatctgaaaatgtactggc | 80 | Qy |
| 1845 | cagaaatgttcaaaatcatagttttaatgtgttttgaaaaggccacacaattatacttta | 7 | DЬ |
| 1800 | agaaatgttcaaaatcatagttttaatgtgttttgaaaaggccacacaattatacttta | 1741 | Qy |
| 1785 | tttgggctaaattatatgtaca | 7 | DЬ |
| | acaaaagggaagacggtaacaatggtcacttcaaactttttgggctaaaattatatgtaca | 1681 | Qy |
| 1725 | ggagtgactttttctcctcgaattgaaacaagtctatggcaaaagaagctgcatttttt | 1666 | DЪ |
| 1680 | gagtgactttttctcctcgaattgaaacaagtctatggcaaaagaagctgcatttttt | 6 | Qy |
| 1665 | cccagaaatgatgttgcattttttgctttagcctgataattgaaactttcaacaatctct | 1606 | Db |
| 1620 | ccagaaatgatgttgcattttttgctttagcctgataattgaaactttcaacaatctc | 1561 | Qy |
| 1605 | tccctgctgtaggcatcagttatgtggtttatgaaaatatgaagcaaactttaggagtaa | 1546 | Db |
| 1560 | ccctgctgtaggcatcagttatgtggtttatgaaaatatgaagcaaactttaggagtaa | 50 | Qy |
| 1545 | tttocaaagaaggaataccaggactttacagaggcatcaccccaaacttcatgaaggtgc | 4 | Db |
| 1500 | ttccaaagaaggaataccaggactttacagaggcatcaccccaaacttcatgaaggtgc | 44 | Qy. |
| 4 | | N | Db |
| 1440 | tcaagccatgttagaaggttccccacagctgaatatggttggcctctttcgacgaatta | 38 | Qy |
| 42 | | 36 | , Db |
| 1380 | cagcacctgtggtcagctggccagctacccattggctttggtgagaactcgcatgcagg | 1321 | 0у |

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Sequence 8162, Application US/09652918
(GENERAL INFORMATION:
APPLICANT: Galvin, Katherine
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLE
ITITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1187-001
CURRENT APPLICATION NUMBER: US/09/652,918
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,130
PRIOR FILING DATE: 1999-08-30
PRIOR FILING DATE: 1999-08-30
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ORGANISM: Homo
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RESULT 7
US-09-667-617-1724
; Sequence 1724, Application U
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Dougl
; APPLICANT: Gearing, David
; TITLE OF INVENTION: NOVEL
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; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1198-001
; CURRENT APPLICATION NUMBER: US/99/667,61
; CURRENT FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/155,295
; PRIOR FILLING DATE: 1999-09-21
; NUMBER OF SEQ ID NOS: 2254
; SOFTWARE: FRASTSEQ for Windows Version 4
; SEQ ID NO 1724
; SEQ ID NO 1724
; SEQ ID NO 1724
; ORGANISM: HOMO Saplens
; ORGANISM: HOMO Saplens
US-09-667-617-1724
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Query Match 94.3 Best Local Similarity 99.3 Matches 2549; Conservative

94.2%;

Score 2517.4; Pred. No. 0; 0; Mismatches

DВ 16;

3545; 2

Indels Length

2;

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; LENGTH: 3545
; TYPE: DNA
; ORGANISM: Homo sa
US-09-698-010-12652
                        CURRENT APPLICATION NUMBER: US/09/698,01
CURRENT FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: 600/162,358
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 15684
SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 12652
LENGTH: 3545
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                                                                                        APPLICANT: Williamson, Mark
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: NOVEL NUCLEIC
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2029-001
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RESULT 9
US-09-710-285-1759
; Sequence 1759, Ap
; GENERAL INFORMATI
                                                                                                                                                                                                     APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Michael J.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID P.
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2006-001
CURRENT APPLICATION NUMBER: US/09/710,289
CURRENT FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: 60/164,507
PRIOR FILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 2347
SOFTMARE: FastSEQ for Windows Version 4.
SEQ ID NO 1759
TYPE: DNA
CORGANISM: Homo sapiens
US-09-710-285-1759
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APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2016-001
CURRENT APPLICATION NUMBER: US/09/726,81
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/168,017
PRIOR APPLICATION NUMBER: 50/168,017
PRIOR FILING DATE: 1999-11-30
NUMBER OF SEQ ID NOS: 3398
SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 3387
LENGTH: 3545
TYPE: DNA
ORGANISM: Homo sapiens
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US-60-213-360-3302

Sequence 3302, Application US/60213360

GENERAL INFORMATION:

APPLICANT: MORTIS, MacDonald

APPLICANT: Lal, Preeti

APPLICANT: Diep, Dinh

TITLE OF INVENTION: Method for the Identi

TITLE OF INVENTION: Polynucleotide Sequen

TITLE OF INVENTION: Identified Thereby

FILE REFERENCE: GX-0014 p

CURRENT APPLICATION NUMBER: US/60/213,360

CURRENT FILING DATE: 2000-06-21
                                 US/60/213,360
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; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PERL Program
; SEQ ID NO 3302
; LENGTH: 3446
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyt
US-60-213-360-3302
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APPLICANT: MORTIS, MacDonald
APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
FITTLE OF INVENTION: METHOD FOR THE ID
TITLE OF INVENTION: POLYMUCLEOTIDE S
TITLE OF INVENTION: POLYMURPHISMS ID
FILE REFERENCE: GX-0019-1 P
CURRENT APPLICATION NUMBER: US/60/324
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 35862
SOFTWARE: PERL Program
SEQ ID NO 14440
LENGTH: 3446
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                                                                                                                      FEATURE:

NAME/KEY: misc_feature
OTHER INFORMATION: Incyte
-60-324-185-14440
                                                                                                                                                             ORGANISM: Homo sapiens
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FILE REFERENCE: GX 0007 p
CURRENT APPLICATION NUMBER: US/60/172,360
CURRENT FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 29838
SOFTWARE: PERL Program
SEQ ID NO 23662
LENGTH: 3393
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 221299.1
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| 60 c | | aagtggattgatcatgagcaagtgatgggctttatttctccctcactggtg |
| 20 c | | tgaacttgctgtttgcaatatgggcagccacaaagggggagaga 2567 |

RESULT 14
US-60-278-561-5850
; Sequence 5850, Application US/60278561
; GENERAL INFORMATION:

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; TYPE: DNA; ORGANISM: Homo sapiens; FEATURE: NAME/KEY: misc_feature; OTHER IMFORMATION: IncytUS-60-278-561-5850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Morris, MacDonald
APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
TITLE OF INVENTION: Method for the Ider
TITLE OF INVENTION: Polymucleotide Sec
TITLE OF INVENTION: Polymorphisms Ider
FILE REFERENCE: GX-0012-1 p
CURRENT APPLICATION NUMBER: US/60/278,
CURRENT APPLICATION NUMBER: US/60/278,
UMMBER OF SEQ ID NOS: 15598
SOFTWARE: PERL Program
SOFTWARE: PERL Program
SEQ ID NO 5850
LENGTH: 3446
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Sequence 755, Application PC/TUS0104098A
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL Nucleic Acids and Po
FILE REFERENCE: 21272-029
CURRENT APPLICATION NUMBER: PCT/US01/04098A
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: Not Yet Assigned
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 09/728,422
PRIOR APPLICATION NUMBER: 09/69,325
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 09/63,561
PRIOR FILING DATE: 2000-09/63,561
PRIOR APPLICATION NUMBER: 09/663,561
PRIOR APPLICATION NUMBER: 09/654,936
PRIOR APPLICATION NUMBER: 09/654,936
PRIOR APPLICATION NUMBER: 09/654,936
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 09/654,936
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 09/520,325
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: 09/598,075
PRIOR APPLICATION NUMBER: 09/560,875
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Best Local Similarity
Matches 2468; Conserv
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| 198 196 | tatgocagttootttatatttaaatttottgttttatatattttgaatgtotttatagat | 1928 1903 | Qy Db |
|------------|--|--------------|----------|
| | aaatttgttttgtgtgttagagttataaatcattaatctttatttcgggtggtttacgtt | 1868 1843 | Qу Db |
| ь н | ttaataatcctgcaaatctctgccctgaatccgaaatctgaaaatgtactggcttgaaca | 1808 1783 | Qу Дъ |
| سو سو | gttcaaaatcatagttttaatgtgttttgaaaaggccacacaaattatacttttatcttttc | 1748 1723 | Фр |
| - - | gggaagacggtaacaatggtcacttcaaacttttgggctaaattatatgtacacagaaat | 1688 1663 | Qу рь |
| | ctttttctcctcgaattgaaacaagtctatggcaaaagaagctgcatttttttcacaaaa | 1628 1603 | Оу |
| <u> </u> | atgatgttgcattttttgctttagcctgataattgaaactttcaaccaatctctggagtga | 1568 1543 | Qу ДЪ |
| 15 | tgtaggcatcagttatgtggtttatgaaaatatgaagcaaactttaggagtaacccagaa | 1508 1483 | Qу |
| 15 14 | agaaggaataccaggactttacagaggcatcaccccaaacttcatgaaggtgctccctgc | 1448 1423 | Qу |
| 14 | catgttagaaggttccccacagctgaatatggttggcctctttcgacgaattatttccaa | 1388 1363 | , Db |
| μ μ α α | ctgtggtcagctggccagctacccattggctttggtgagaactcgcatgcaggctcaagc | 1328 1303 | Оу |
| 1 1 | aaaagattctgtaaaccctggagtcatggtgttgctgggatgcggtgccttatccagcac | 1268 1243 | Qy Db |
| <u> </u> | 3 tgcaggcatagatcttgctgtgtatgagctcttgaagtcctattggctggataattttgc | 1208 1183 | Оу |
| <u> </u> | tgaaggcttgggagctttttacaaaggctatgttcccaatttattaggtatcatacctta | 1148 1123 | Qу |
| ـ ــ | tgtaggcaaaactgggcagtactctggaatatatgattgtgccaagaagattttgaaaca | 1088 | Qу |
| р р | 3 gyctgyaycaactycacayacttttatatatccaatgyaygttatyaaaaccayyctyyc | 1028 | Оy |
| | 3 gttacttactgaagaaggacaaaaaataggaacatttgagagatttattt | 968 943 | рь |
| 9 9 | gtcatcaaaattgctcctgagacagctgttaaattctgggcatatgaacagtacaagaa | 908 | Qу |
| | | | |

| Qу Дъ | Оy | Qy Db | Qу Дъ | Qy Db | Qу ДЪ | Qу ДЪ | Qy Db | Qy Db | Db |
|---|--|---|---|---|---|---|---|--|------|
| 2528 2501 | 2468 2443 | 2408 2383 | 2348 2323 | 2288 2263 | 2228 2203 | 2168 2143 | 2108 2083 | 2048 2023 | 1963 |
| cttgctgtttgcaatatgggcagccacaaagggggagaga 2567 | gattgatcatgagcaagtgatgggctttatttctccctcactggtgaatatcctttgaa 2527 | aggaagacttettgggaccattettagtaacetgaaatttettttttaattgcatgaagt 2467 | gcatctttgttttcctttgtcctttgtttcctaccttttgaatcagattccgttttagtc 2407 | gccattgctttgaaaagcagcaggaaacgaaattttttgacttgtatcagcttctgcaga 2347 | agtatattactgttaaattaccaacacaaggcaatttattt | gcacttttccattttaccactgtaccattatttggttcctggagttatacactaattttc 2227 |) gaatgaacacagtggtggaatttotgaagggaagtgatgaaattatatttatt | cagcaaaagcatccaaataagtatagggtttatgtccttatttttctttc | |

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4478, Ap
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TITLE OF INVENTION: NUCLEIC ACID MOLECULES E
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLOO1103
...CURRENT APPLICATION NUMBER: US/09/777,921A
CURRENT APPLICATION NUMBER: US/09/777,921A
CURRENT FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 126
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
SEQ ID NO 1
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LENGTH: 2673
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| | 77921A | ALIGNMENTS | -10-063-553- | -10-063-551- | -10-063-550- | -10-063-549- | -10-063-548- | -10-063-547- | 10-063-546- | 10-063-544- | 10-063-541- | 10-063-540- | 10-063-560- | 10-063-536- | 10-063-534- | 10-063-532- | 10-063-530- | 10-063-529- | 10-063-528- | 10-063-527- | 10-063-526- | 10-063-525- | |
| 57, 57, 57, 57, 57, 57, 57, 57, 57, 57, | | | | | | | | | | | | | | | | | | | 57, Appl | | 57, Appl | , Appl | |

; LENGTH: 2673 ; TYPE: DNA ; ORGANISM: Homo s US-09-777-921A-1 Query Match
Best Local Similarity
Matches 2673; Conserv tgggccaggacgccgaggagaaaatttttactactggagatgtcaacaacgatgggaagc gccaggacgcggagcagccgacgcgctacgagaccctcttccaggcactggaccgcaatg gcgctggtcccggtctcgccccgcagccctcgatctccccgtgacttcctcggccaggccg gggacggagtggtggacatcggcgagctgcaggaaggggctcaggaacctgggcatccctc cctgcgcctctgggaccatgttgcgctggctgcggggacttcgcgctgcccaccgcggcct tgggccaggacgccgaggaaaatttttactactggagatgtcaacaaagatgggaagc gccaggacgcggagcagccgacgcgctacgagaccctcttccaggcactggaccgcaatg cctgcgcctctgggaccatgttgcgctggctgcggacttcgcgctgcccaccgcggcct 180 gcgctggtcccggtctcgccccgcagccctcgatctcccgtgacttcctcggccaggccg 100.0%; Score 2673; llarity 100.0%; Pred. No. 0; Conservative 0; Mismatches DB 5 Length 2673; 0; Gaps 300 240 120 60 60 0

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| 10 | QY 1381 ctcaagccatgttagaaggttccccacagctgaatatggttggcctctttcgacgaatta 144 | ם ם |
| 80 | 21 ccagcacctgtggtcagctggccagctacccattggctttggtgagaactcgcatgcagg 13 | ם ט |
| 20 | Qy 1261 attttgcaaaagattctgtaaaccctggagtcatggtgttgctgggatgcggtgccttat 13 | ם ס |
| 60 | Oy 1201 taccttatgcaggcatagatcttgctgtgtatgagctcttgaagtcctattggctggata 12 | U 0 |
| 0 00 | Qy 1141 tgaaacatgaaggcttgggagctttttacaaaggctatgttcccaatttattaggtatca 12 | U 0 |
| 40 0 | Oy 1081 ggctggctgtaggcaaaactgggcagtactctggaatatatgattgttgccaagaagattt 114 | п о |
| 80 | Oy 1021 gttccatggctggagcaactgcacagacttttatatatccaatggaggttatgaaaacca 10 | U 0 |
| 20 | Qy 961 acaagaagttacttactgaagaaggacaaaaaaataggaacatttgagagatttattt | ם ם |
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| | Oy 361 tggattttgaagaatttatgaagtaccttaaagaccatgagaagaaaatgaaaattggcat 42 | U 0 |

| 2580 | ctttgaacttgctgtttgcaatatgggcagccacaaagggggagagatgcctattaaatc | 2521 | Qy |
|------|--|------|------------|
| 2520 | tgaagtggattgatcatgagcaagtgatgggctttatttctccctcactggtgaatat | 2461 | рь |
| 2520 | atgaagtggaftgatcatgagcaagtgatgggctftaftfctccctcactggfgaatafc | 2461 | Qy |
| 46 | ttagtcaggaagacttcttgggaccattcttagtaacctgaaatttcttttttaattgc | | Db |
| 46 | thadroagaaaachtottagaacoattottagtaacotgaattotttttaattac | 4 | 0 1 |
| 2400 | <pre>ctgcagagcatctttgttttcctttgtcctttgtttcctaccttttgaatcagattccgt </pre> | 2341 | p dq Qy |
| . iŭ | tatcctgccattgctttgaaaagcagcaggaaacgaaattttttgacttgtatcagctt | 28 | Db |
| | | 28 | Qy |
| 2280 | the desired the second case of the second cases of the second case of the second cases | 2221 | Db |
| 2280 | attttcagtatattactgttaaattaccaacacaaggcaatttattt | 2221 | Qy |
| 2220 | tcagtgggcacttttccattttaccactgtaccattatttggttcctggagttatacact | 2161 | ф |
| 2220 | cagtgggcacttttccattttaccactgtaccattatttggttcctggagttatacact | 2161 | Оу |
| 2160 | tgaatacgaatgaacacagtggtggaatttctgaagggaagtgatgaaattatatttatt | 2101 | ДĎ |
| 2160 | gaatacgaatgaacacagtggtggaattttctgaagggaagtgatgaaattatatttatt | 2101 | Qy |
| 2100 | taccttacagcaaaagcatccaaataagtatagggtttatgtccttattttctttc | 2041 | Db |
| 2100 | accttacagcaaaagcatccaaataagtatagggtttatgtccttatttttctttc | 2041 | Qy |
| 2040 | tatagatttctttaaatttccttatagaaccattaatagaaaatcattacatttaaaata | 1981 | DЪ |
| 2040 | atagatttctttaaatttccttatagaaccattaatagaaaatcattacatttaaaata | 1981 | Qy |
| 1980 | tacgtttatgccagttcctttatatttaaatttcttgttttatatata | 1921 | Db |
| 1980 | tacgtttatgccagttcctttatatttaaatttcttgttttatatattttgaatgtctt | 1921 | Qy |
| 1920 | tgaacaaaatttgttttgtgtgtttagagttataaatcattaatctttatttcgggtggt | 1861 | Db |
| 1920 | tgaacaaaatttgttttgtgtgttagagttataaatcattaatctttatttcgggtggt | 1861 | Qy |
| 1860 | tottttottaataatcotgcaaatctotgccotgaatcogaaatctgaaaatgtactggc | 1801 | Дb |
| 1860 | cttttcttaataatcctgcaaatctctgccctgaatccgaaatctgaaaatgtactggc | 1801 | Qy |
| 1800 | cagaaatgttcaaaatcatagttttaatgtgttttgaaaaggccacacaattatacttta | 1741 | σb |
| 1800 | agaaatgttcaaaatcatagttttaatgtgttttgaaaaggccacacaattatacttta | 1741 | Qy |
| 1740 | cacaaaagggaagacggtaacaatggtcacttcaaacttttgggctaaattatatgtaca | 1681 | Db |
| 1740 | acaaaagggaagacggtaacaatggtcacttcaaacttttgggctaaattatatgtaca | 1681 | Qy |
| 1680 | ggagtgactttttctcctcgaattgaaacaagtctatggcaaaagaagctgcatttttt | 1621 | Дb |
| 1680 | gagtgactttttctcctcgaattgaaacaagtctatggcaaaagaagctgcattttttt | 1621 | Qy |
| 1620 | cccagaaatgatgttgcattttttgctttagcctgataattgaaactttcaacaatctct | 1561 | Дb |
| 1620 | ccagaaatgatgttgcattttttgctttagcctgataattgaaactttcaacaatctct | 1561 | Qy |
| 56 | | ίσ | Db - |
| 1560 | .ccctgctgtaggcatcagttatgtggtttatgaaaatatgaagcaaactttaggagtaa | 1501 | Qy |
| 1500 | | 1441 | Db |

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PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 419
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 408
LENGTH: 3384
TYPE: No.
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US-09-620-325-408
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APPLICANT: Tillinghast, John
APPLICANT: Drimanac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids :
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 787C1P2B
CURRENT APPLICATION NUMBER: US/09/620,32:
CURRENT FILING DATE: 2000-04-27
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Best L
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                                                                                                                                                                                                                     Matches
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LOCATION: (113)..(1546)
-09-620-325-408
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Local Similarity 98.7
hes 2468; Conservative
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                                                                    cgcggagcagccgacgcgctacgagaccctcttccaggcactggaccgcaatggggacgg
                                                                                                                                                                                 INFORMATION:
 ggacgccgaggagaaaatttttactactggagatgtcaacaaagatgggaagctggattt
                        agtggtggacatcggcgagctgcaggagggctcaggaacctgggcatccctctgggcca
                                     agtggtggacatcggcgagctgcaggagggctcaggaacctgggcatccctctgggcca
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Ma, Yunqing
Wang, Dunrui
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Zhang, Jie
Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A.
Xue, Aidong J.
Yang, Yonghong
Wehrman, Tom
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Wang, Jian-Rui
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Liu, Chenghua
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Pred. No. 0;
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Sequence 3, Application US/09777921A
GENERAL INFORMATION:
APPLICANT: MERKULOV et al.
ITITLE OF INVENTION: NUCLEIC ACID MOLECULES E
TITLE OF INVENTION: NUCLEIC ACID MOLECULES E
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001103
CURRENT APPLICATION NUMBER: US/09/777,921A
CURRENT APPLICATION NUMBER: US/09/777,921A
CURRENT FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 126
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO
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: LOCATION: (1)...(69327)
: OTHER INFORMATION: n = 1
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Best Local Similarity 98.6
Matches 1166; Conservative
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TYPE: DNA
ORGANISM: HOMO
FEATURE:
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SOFTWARE: FastSEQ for Windows
SEQ ID NO 4478
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Sequence 4478, Application US/09919002
GENERAL INFORMATION:
                                                             Matches
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APPLICANT: Liu, Jin
TITLE OF INVENTION: NOVEL CONTIGS
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 20411-752CON1
                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/919,002
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: APPLICATION NUMBER:
PRIOR FILING DATE: FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: APPLICATION NUMBER:
PRIOR FILING DATE: FILING DATE: 1998-02-13
                                                                                                                                ORGANISM: Homo
09-919-002-4478
                                                                                                                                                          SEQ ID NO 4478
LENGTH: 1839
TYPE: DNA
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976; Conserv
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                                                        Score 933.4; DB 5;
Pred. No. 4.1e-182;
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Sequence 38, Application US/1 GENERAL INFORMATION: APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic FILE REFERENCE: PJZ05C1

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CURRENT FILING DATE: 2002-06-12
Prior Application removed - See File Wrapp
NUMBER OF SEQ ID NOS: 384
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 38
LENGTH: 757
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LOCATION: (659)
OTHER INFORMATION: n equ
FEATURE:
NAME/KEY: misc_feature
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ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
LOCATION: (80)
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OTHER INFORMATION: n equals
10-158-057-38
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SOFTWARE: FastSEQ for W
SEQ ID NO 120
LENGTH: 601
TYPE: DNA
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US-09-777-921A-120
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GENERAL INFORMATION:
APPLICANT: MERKULOV et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUM
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001103
CURRENT APPLICATION NUMBER: US/09/777,921A
CURRENT FILING DATE: 2002-02-07
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Best Local Similarity
Matches 598; Conserv
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RESULT 7 US-09-777-921A-121

Sequence 121,

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2139

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TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: AND USES THEREOF
FILE REPERENCE: CL001103
CURRENT APPLICATION NUMBER: US/09/777,921A
CURRENT FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 126
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: MERKULOV et al
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99.5%;
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Pred. No. 3.3e-113;
1; Mismatches 2;
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CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: 09/866,050
PRIOR FILING DATE: 2001-05-24
PRIOR PRIOR PAPLICATION NUMBER: 60/221,232
PRIOR FILING DATE: 2000-07-25
PRIOR PAPLICATION NUMBER: 60/2206,650
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: 09/312,283
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: PCT/NZ99/00051
PRIOR APPLICATION NUMBER: 97/188,930
PRIOR FILING DATE: 1998-11-09
PRIOR APPLICATION NUMBER: 09/069,726
PRIOR RILING DATE: 1988-11-09
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Best Local Similarity
Matches 807; Conserv
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; LENGTH: 601 ; TYPE: DNA ; ORGANISM: Homo : US-09-777-921A-121

sapiens

Matches Query Match Best Local

hes 598;

Similarity

1874

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RESULT 9
US-09-312-283B-262
US-09-312-283B-262
Sequence 262, Application US/09312283B
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated
TITLE OF INVENTION: and Methods for The
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,28:
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; NUMBER OF SEQ ID NO; SOFTWARE: FastSEQ I SEQ ID NO 262; SEQ ID NO 262; LENGTH: 1816; TYPE: DNA GONAISM: MOUSE US-09-312-283B-262
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Pred. No. 2.2e-102;
0; Mismatches 436;
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APPLICANT: ONCURENT, PROCUREW
APPLICANT: MUTISON, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated Fr
TITLE OF INVENTION: and Methods for Their U
FILE REFERENCE: 11000.1011c5
CURRENT APPLICATION NUMBER: US/10/152,661
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: 60/221,232
PRIOR APPLICATION NUMBER: 60/221,232
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: 60/206,650
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: 09/312,283
PRIOR FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: 09/188,930
PRIOR APPLICATION NUMBER: 09/069,726
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; ORGANISM: Mouse
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US-10-152-661-262
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SEQ ID NO 262
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                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 19 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                  Q ID NO 262
LENGTH: 1816
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Sleeman, Matthew
Onrust, Rene
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                                                                                                                                               Score 545.4; DB 7;
Pred. No. 2.2e-102;
0; Mismatches 436;
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TITLE OF INVENTION: Secreted and Tra
TITLE OF INVENTION: Acids Encoding
FILE REFERENCE: P2730P1C48
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CURRENT FILING DATE: 2001-11-16
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RESULT 12 US-10-063-502-57 Sequence 57, Application GENERAL INFORMATION: APPLICANT:
APPLICANT: APPLICANT: Eaton, Dan I Filvaroff, Goddard, Audrey Godowski, Paul Gerritsen, Mary ,Ellen us/10063502 H

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; ORGANISM: Homo
US-10-063-502-57
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CURRENT APPLICATION NUMBER: US/10/063,502
CURRENT FILING DATE: 2002-05-01
Prior Application removed - See File Wrapper or NUMBER OF SEQ ID NOS: 170
SEQ ID NO 57
LENGTH: 3334
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Best Local Similarity 64.8%;
Matches 806; Conservative
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Pred. No. 5.
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; ORGANISM: Homo
US-10-063-510-57
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Best Local Similarity
                                                                                                                                                                                                                                               SEQ ID NO 57
LENGTH: 3334
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APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                         FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,510
CURRENT FILING DATE: 2002-05-01
                                                                                                                                                                                                                                                                             Prior Application removed - NUMBER OF SEQ ID NOS: 170
                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gurney, Austin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
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ttgtccattatctccaagatcatgagaagaagctgaggctggtgtttaagattttggaca
                                                            agcagaaaattgtacaagctggagataaggaccttgatgggcagctagactttgaagaat
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Grimaldi,Christopher
                                                                                                                         Conservative
                                                                                                                                      20.3%;
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                                                                                                                                                                                                                                                                                             See File Wrapper
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                                                                                                                        Score 543.8; DB 7;
Pred. No. 5.6e-102;
0; Mismatches 437;
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Best Local S
Matches 806
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,512
CURRENT FILING DATE: 2002-05-01
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 170
SEQ ID NO 57
LENGTH: 3334
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Grimaldi, Christopher
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Goddard, Audrey
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US-10-063-513-57, Ap. GENERAL INFORMAL APPLICANT: Eat. APPLICANT: F1 APPLICANT: GO APPLICANT: GO APPLICANT: GO APPLICANT: GO APPLICANT: GO APPLICANT: GO APPLICANT: GO
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APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary E.
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gunney, Austin L.
APPLICANT: Wartanabe, Colin K.
APPLICANT: Wartanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRA
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE REFERENCE: P323ORIC1
CURRENT APPLICATION UNMBER: US/10/063,513
CURRENT EILING DATE: 2002-05-01
; TYPE: DNA
; ORGANISM: HOMO
US-10-063-513-57
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                                               SEQ ID NO 57
LENGTH: 3334
                                                                           Prior Application removed
NUMBER OF SEQ ID NOS: 170
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Search completed: August 18, 2002, 09:22:57 Job time: 7561 sec

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2: /cgn2_6/ptcodata/1/paa/US07_COMB.pep:*

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4: /cgn2_6/ptcodata/1/paa/US081_COMB.pep:*

5: /cgn2_6/ptcodata/1/paa/US082_COMB.pep:*

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Copyright (c) 1993 - 2000 Comp
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| NO. SO | Score 2481 2471 2373 | Query Match Length DB 100.0 477 21 99.6 477 1 95.6 475 21 | ength 477 477 475 | 21 21 21 | DB ID 21 US-09-777-921-2 1 PCT-US01-04098A-1739 21 US-09-777-921-4 |
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| 4. | ٥, | 90.5 | 470 | Н | PCT-US01-14827-10548 |
| σ | ٥ | 85.9 | 410 | 21 | US-09-777-921-5 |
| 6 | | 71.8 | 342 | 21 | US-09-777-921-6 |
| 7 | _ | 62.9 | 300 | Н | 1 PCT-US01-21148-6 |

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ALIGNMENTS

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RESULT 1
US-09-777-921-2
: Sequence 2, Application US/09777921
: Sequence 2, Application US/09777921
: GENERAL INFORMATION:
APPLICANT: MERKULOV et al
: TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: MUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
: TITLE OF INVENTION: AND USES THEREOF
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PRIOR APPLICATION NUMBER: 09/728,422
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 09/693,325
PRIOR APPLICATION NUMBER: 09/693,325
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/63,561
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/620,325
PRIOR APPLICATION NUMBER: 09/620,325
PRIOR APPLICATION NUMBER: 09/620,325
PRIOR FILING DATE: 2000-09-11
PRIOR APPLICATION NUMBER: 09/598,075
PRIOR FILING DATE: 2000-6-20
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER: OF SEQ ID NO 1739
LENGTH: 477
TYPE: DET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides FILE REFERENCE: 21272-029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hyseq,
                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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                      MVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGA
 EKIFTTGDVNKDGKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGL
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Pred. No. 1.8e-213;
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NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: CL001103
CURRENT APPLICATION NUMBER: US/09/777,921
CURRENT FILING DATE: 2001-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MERKULOV et al TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS, TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                    MLRWLRGFVLPTAACQGAEPPTRYETLFQALDRNGDGVVDIRELQEGLKSLGIPLGQDAE
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TAQTFIYPMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGI
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Pred. No. 1.3e-204;
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OTHER INFORMATION: MITOCHONDRIAL CARRIER PROTEIN SIGNATURE domain identified
OTHER INFORMATION: eMATRIX, accession number PR00926F, p-value=7.750e-19, raw
OTHER INFORMATION: 17.75
NAME/KEY: DOMAIN
LOCATION: (222)..(466)
OTHER INFORMATION: Mitochondrial carrier proteins domain identified by PFam,
OTHER INFORMATION: accession name mito_carr, E-value=7.2e-71, PFam score of 2
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PCT-USO1-14827-10548
; Sequence 10548, Application
; GENERAL INFORMATION:
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Best Local Sim
Matches 436;
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SOFTWARE: Custom
SEQ ID NO 10548
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 21272-104
CURRENT APPLICATION NUMBER: PCT/US01/14827
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/577,408
PRIOR FILING DATE: 2000-05-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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             DLAVYELLKSYWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLE
                                                     MVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGA
                                                                                                                                                                   EKIFTTGDVNKDGKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGL 120
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                                                                                                               MVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQ-----
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91.4%; Pred. No. 3.6e-193;
tive 2; Mismatches 3;
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US-09-777-921-5

Sequence 5, Application US/09777921

GENERAL INFORMATION:
APPLICANT: MERKULOV et al

TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001103

CURRENT APPLICATION NUMBER: US/09/777,921

CURRENT FILING DATE: 2001-07-02

NUMBER OF SEO ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO

SEQ ID NO

LENGTH: 410
Sequence 6, Application US/09777921

GENERAL INFORMATION:
APPLICANT: MERKULOV et al
APPLICANT: MERKULOV et al
ITITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
ITITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
ITITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001103
CURRENT APPLICATION NUMBER: US/09/777,921
CURRENT FILING DATE: 2001-07-02
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 342
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US-09-777-921-5
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Best Local Similarity
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HUMAN TRANSPORTER

PROTEINS

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APPLICANT: MERKULOV, Gennady et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000723PCT
CURRENT APPLICATION NUMBER: PCT/US01/21148
CURRENT FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: 60/216,340
PRIOR APPLICATION NUMBER: 60/216,340
PRIOR APPLICATION NUMBER: 09/810,673
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; ORGANISM: Human
US-09-777-921-6
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PCT-US01-21148-6
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                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version SEQ ID NO 6 .
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Best Local
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   121
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nes 342; Conserv
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   DGTMTVDWNEWRDYFLFNPVTDIEEIIRFWKHSTGIDIGDSLTIPDEFTEDEKKSGQWWR
                DGTMTVDWNEWRDXFLFNPVTDIEEIIRFWKHSTGIDIGDSLTIPDEFTEDEKKSGQWWR 196
                                                                           FEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQAELILQSIDV
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                                                             FEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQAELILQSIDV
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                                                                                                                                                                                                   Score 1560; DB 1; Pred. No. 1.3e-131;
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CURRENT APPLICATION NUMBER: PCT/US01/04926A
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 09/664,641
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-16,807
PRIOR APPLICATION NUMBER: 09/516,807
PRIOR APPLICATION NUMBER: 09/597,707
PRIOR APPLICATION NUMBER: 09/597,707
PRIOR FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: 09/577,409
PRIOR APPLICATION NUMBER: 09/517,409
PRIOR APPLICATION NUMBER: 09/515,126
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PCT-US01-04926A-194
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US-09-810-673A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/09810673A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                Sequence 194, Application PC/TUS0104926A GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MERKULOV, Gennady et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUW
TITLE OF INVENTION: AND USES THERBOF
FILE REFERENCE: CL000723
                                                                                                                                                                                                          TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides FILE REFERENCE: 21272-041
                                                                                                                                                                                                                                               APPLICANT: Hyseq,
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                  257
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                                                                                                                                                                                                                                                                                                                                                                              241 NVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIYPMEVMKTRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQAELILQSIDV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                     QLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQMVKEGGIRSLWRGNGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QLLAGG IAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQMVKEGGIRSLWRGNGT
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                                                                                                                                                                                                                                               Inc.
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 Mismatches

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CURRENT APPLICATION NUMBER: PCT/US01/04926A
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 09/664,641
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/616,807
PRIOR APPLICATION NUMBER: 09/616,807
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 09/597,707
PRIOR APPLICATION NUMBER: 09/577,409
PRIOR FILING DATE: 2000-06-18
PRIOR FILING DATE: 2000-05-18
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; ORGANISM: HOMO PCT-US01-04926A-538
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                                                                                                                                                                                                                                                                                                                               PCT-US01-04926A-538
                        SEQ ID NO 538
LENGTH: 509
TYPE: PRT
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NUMBER OF SEQ ID NOS: 688
SOFTWARE: CUSTOM
SEQ ID NO 194
LENGTH: 471
                                                                                                                                                                                                                                                                                                     Sequence 538, Applic GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                          APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-041
                                                                NUMBER OF SEQ ID SOFTWARE: Custom
                                                                                            PRIOR APPLICATION NUMBER: 09/515,126 PRIOR FILING DATE: 2000-02-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMDRDGTMTIDWQEWRDHFLLHSLENVEDVLYFWKHSTVLDIGECLTVPDEFSKQEKLTG
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61.5%;
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Pred. No. 1.3e~130;
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CURRENT APPLICATION NUMBER: US/09/709, 238
CURRENT APPLICATION NUMBER: PCT/US99/1252
PRIOR APPLICATION NUMBER: PCT/US99/1252
PRIOR FILING DATE: 1999-06-02
PRIOR FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: US 60/087,607
PRIOR APPLICATION NUMBER: US 60/087,609
PRIOR APPLICATION NUMBER: US 60/087,759
PRIOR APPLICATION NUMBER: US 60/087,759
PRIOR FILING DATE: 1998-06-03
PRIOR PRIOR APPLICATION NUMBER: US 60/087,827
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,021
PRIOR FILING DATE: 1998-06-04
PRIOR PRIOR APPLICATION NUMBER: US 60/088,025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 60/088,025
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APPLICANT: Baker, K.
APPLICANT: Chen, Ji.
APPLICANT: Goddard,
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Best Local S
Matches 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 289,
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wood, WAPPLICANT: Yuan, JUSTITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 GNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIYPMEVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 QWWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQMVKEGGIRSLWR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222 MWWKQLVAGAVAGAVSRTGTAPLDRLKVFMQVHASKTNRLNILGGLRSMVLEGGIRSLWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 GGLDLEEFSRYLQEREQRLLLMFHSLDRNQDGHIDVSEIQQSFRALGISISLEQAEKILH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 DAERRORWGRLFEELDSNKDGRVDVHELROGLARLG---GGNPDPGAQQGISSEGDADPD 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 61.9 nes 286; Conservative
R FILING DATE: 1998-06
R APPLICATION NUMBER:
R FILING DATE: 1998-06
R APPLICATION NUMBER:
R APPLICATION NUMBER:
R FILING DATE: 1998-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KTRLTLRRTGQYKGLLDCARRILEREGPRAFYRGYLPNVLGIIPYAGIDLAVYETLKNWW
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gurney, Austin
Smith, Victoria
Watanabe, Colin K
Wood, William I.
Yuan, Jean
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baker, Kevin
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                              UMBER: US 60/088,028
1998-06-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.6%; Score 1552.5; DB 1 61.5%; Pred. No. 1.5e-130;
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                    60/088,029
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OR FILING DATE: 1998-06-10
RAPPLICATION NUMBER: US 60/088,741
DR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: US 60/088,742
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: US 60/088,810
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OR APPLICATION NUMBER: US 60/088,810

OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: US 60/088,730
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OR APPLICATION NUMBER: US 60/088,734
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: US 60/088,738
OR APPLICATION NUMBER: US 60/088,738
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: US 60/088,740
OR FILING DATE: 1998-06-10
OR FILING DATE: 1998-06-10

APPLICATION NUMBER: FILING DATE: 1998-

US 60/088,722

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OR APPLICATION NUMBER:

OR FILING DATE:

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IOR APPLICATION NUMBER:

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PTI.ING DATE:

1998-06-10

US 60/088,825

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APPLICATION NUMBER:

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OR FILING DATE: 1998-06-05
OR APPLICATION NUMBER: US 60/088,202
OR APPLICATION NUMBER: US 60/088,212
OR APPLICATION NUMBER: US 60/088,212
OR FILING DATE: 1998-06-05
OR APPLICATION NUMBER: US 60/088,217
OR ETLING DATE: 1998-06-05
OR FILING DATE: 1998-06-09
OR PPLICATION NUMBER: US 60/088,655
OR FILING DATE: 1998-06-09

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N NUMBER: US 60/088,030 TE: 1998-06-04 N NUMBER: US 60/088,033 TE: 1998-06-04 TE: 1998-06-04 US 60/088,326

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DR FILING DATE: 1998-06-11

PR APPLICATION NUMBER: US 60

PR FILING DATE: 1998-06-12

PR APPLICATION NUMBER: US 60

PR FILING DATE: 1998-06-12

PR FILING DATE: 1998-06-16

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Sequence 289, Application US/09941992
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J
APPLICANT: Baker, Kevin P
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Beton, Dan L
APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
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IOR APPLICATION NUMBER: US 60/091,633
IOR APPLICATION NUMBER: US 60/091,636
IOR FILING DATE: 1998-07-02
IOR APPLICATION NUMBER: US 60/091,673
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IOR APPLICATION NUMBER: US 60/091,673
IOR FILING DATE: 1998-07-07
IOR APPLICATION NUMBER: US 60/091,978
IOR FILING DATE: 1998-07-07
IOR APPLICATION NUMBER: US 60/091,982
IOR FILING DATE: 1998-07-07
IOR APPLICATION NUMBER: US 60/092,182
IOR FILING DATE: 1998-07-09
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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C+=wart, Timothy A.
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PR APPLICATION NUMBER: 60/089532
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RESULT 13
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TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: PZ730P1C56
CURRENT APPLICATION NUMBER: US/09/989,279
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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OR APPLICATION NUMBER: 60/084600
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APPLICATION NUMBER: 60/083322
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FILING DATE: 1998-02-25
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Grimaldi, J.Christopher
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Roy, Margaret Ann
Stewart, Timothy A.
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CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-17
PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065116
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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TITLE OF INVENTION: Secrete
TITLE OF INVENTION: Acids
FILE REFERENCE: P2730P1C66
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FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/
FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/
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FILING DATE: 1998-02-25
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Stewart, Timothy A.
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APPLICANT: Napier, Mary A.
APPLICANT: Napier, Mary A.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Tumas, Daniel
APPLICANT: Watnabe, Colin K.
APPLICANT: Watnabe, Colin K.
APPLICANT: Wood, William I.
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CUGRENT APPLICATION NUMBER: US/09/989,721
CURRENT FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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Grimaldi, J. Christopher
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Gerritsen, Mary E.
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OR FILING DATE: 1998-06-19
OR APPLICATION NUMBER: 60/089952
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OR APPLICATION NUMBER: 60/090252
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1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

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US-09-797-921A-6
US-09-797-921A-6
US-09-997-150-289
US-10-063-510-58
US-10-063-512-58
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; Sequence 130652, Application U;
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIM
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TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUM
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001103
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SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                    TISEQQAELILQSIDVDGTMTVDWNEWRDYFLFNPVTDIEEIIRFWKHSTGIDIGDSLTI 180
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I: Danzer,
INVENTION:
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PROTEIN
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 FAMILY MEMBE
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FILE REFERENCE: 261/210

CURRENT APPLICATION NUMBER: US/09/791,537

CURRENT FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 153055

SOUTWARE: PAtentin version 3.0

SEQ ID NO 130652

LENGTH: 475

TYPE: PRT

ORCANUTE: 261/210

METHODS OF USE THEREOF
                                                                                     ; TYPE: PRT
; ORGANISM: Homo
US-09-777-921A-5
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US-09-777-921A-5
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Query Match
Best Local S
Matches 409
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APPLICANT: MERKULOV et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUM
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001103
                                                                                                                                                             SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09777921A
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Best Local Similarity
                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/777,921A
CURRENT FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 126
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                        LENGTH: 410
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                  85.9%;
99.8%;
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Score 2132; DB 5;
Pred. No. 2.5e-166;
0; Mismatches 1;
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                                   Length 410;
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GENERAL INFORMATION:

APPLICANT: Bionomix, Inc.

APPLICANT: Debe, Derek

APPLICANT: Debe, Derek

APPLICANT: Debe, Derek

APPLICANT: Debe, Derek

TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF

TITLE OF INVENTION: METHODS OF USE THEREOF

FILE REFERENCE: 261/210

CURRENT APPLICATION NUMBER: US/09/791,537

CURRENT APPLICATION NUMBER: US/09/791,537

CURRENT FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 153055

SOFTWARE: Patentin version 3.0

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                   RSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIY
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                                              EKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKIMMQVHGSKSDKMNIFGGFRQMVKEGGI
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  409;
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99.8%; Pred. No. 2.56
tive 0; Mismatches
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2.5e-166;
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APPLICANT: Warnock, Dale E.

TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION

TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEON

FILE REFERENCE: 660088 465P2

CURRENT APPLICATION NUMBER: US/60/389,987

CURRENT APPLICATION DAMBER: 2002-06-17

NUMBER OF SEQ ID NOS: 3025

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 765

LENGTH: 411
RESULT 7
US-09-777-921A-6
; Sequence 6, Application
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ghosh, s
APPLICANT: Fahy, I
APPLICANT: Zhang,
APPLICANT: Gibson,
APPLICANT: Taylor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 765, Application US/60389987 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                               301
                                                                                                                                                                                                        241
                                                                                                                                                                                                                                 248
                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                      121
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                                                                                                     368 LKSYWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQA 417
                                                                                                                                                                                                                                                                                                                                                 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 RSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIY
                                                                                                                                                                                                                                                                                          188
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                                                                                                                                                              PMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYEL
                                                                                                                                                                                                     RSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIY
                                                                                                                                                                                                                                                          ELILQSIDVDGTMTVDWNEWRDYFLFNPVTDIEEIIRFWKHSTGIDIGDSLTIPDEFTED
                                                                                                                                                                                                                                                                                                                                                                                           DVNKDGKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                   {\tt FVLPTAACQDAEQPTRYETLFQALDRNGDGVVDIGELQEGLRNLGIPLGQDAEEKIFTTG}
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FALPTAACQDAEQPTRYETLFQALDRNGDGVVDIGELQEGLRNLGIPLGQDAEEKIFTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKSYWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYEL
                                                                                                                                                                                                                                                                                                                                                                            DVNKDGKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQA
                                                                                        LKSYWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gibson, Bradford
Taylor, Steven W.
Glenn, Gary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhang, Bing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fahy, Eoin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                 US/09777921A
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Pred. No. 2.5e-166;
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Length Indels

0;

Gaps

0;

67

187

120

180

240

247

300

360

PROTEOME

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RESULT 8
US-09-991-150-289
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                                                                                                                                                                                                                                                                                                                                  Sequence 289, Application GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 342; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 6
LENGTH: 342
                                                                                                               APPLICANT:
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TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUM
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001103
CURRENT FILLORATION NUMBER: US/09/777,921A
CURRENT FILLING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 126
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                     APPLICANT: APPLICANT:
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                               APPLICANT:
                                              APPLICANT:
                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RDYFLFNPVTDIEEIIRFWKHSTGIDIGDSLTIPDEFTEDEKKSGQWWRQLLAGGIAGAV 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIYPMEVMKTRLAVGKTGQYSGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KFWAYEQYKKLLTEEGQKIGTFERFISGSMAGATAQTFIYPMEVMKTRLAVGKTGQYSGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQAELILQSIDVDGTMTVDWNEW 147
                                                                                                                                                      Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                                   Ashkenazi, Avi J.
Watanabe, Colin K. Williams, P. Mickey Wood, William I.
                                                     Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
                                                                                                                             Gurney, Austin L.
Kljavin, Ivar J.
                                              Tumas,
                                                                                                                                                                                                                                 Fong, Sherman
                                                                                                                                                                                                                                                                                                     Baker, Kevin P
                                                                                                   Pan, James
                                                                                                              Napier, Mary A.
                                                                                                                                                                                                                                           Ferrara, Napoleone
                                                                                                                                                                                                                                                            Eaton, Dan L.
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                                        Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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; ORGANISM: Homo Sapien US-10-063-502-58
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                                                                                                                                                                                                                                                                                 Sequence 58,
GENERAL INFO
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                            Prior Application removed
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 58
LENGTH: 469
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 289
LENGTH: 469
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                   APPLICANT: APPLICANT:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Secreted and Transmembrane Polypeptides TITLE OF INVENTION: Acids Encoding the Same EILE REFERENCE: p.7730p1c48

CURRENT APPLICATION NUMBER: US/09/991,150

CURRENT FILING DATE: 2001-11-16

Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 532
                                                                                                                                                TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3230R1C1
                                                                                                                CURRENT APPLICATION NUMBER: US/10/063,502 CURRENT FILING DATE: 2002-05-01
                                                                                                                                                                                                   APPLICANT: APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                       58, Application US/10063502
INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEKIFTTGDVNKDGKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGAPEVIMSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDLAVYELLKSYWLDNFAKDSVNPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAML 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATAQTFIYPMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VPDEFTVEERQTGMWWRHLVAGGGAGAVSRTCTAPLDRLKVLMQVHASRSNNMGIVGGFT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTISEQQAELILQSIDVDGTMTVDWNEWRDYFLFNPVTDIEEIIRFWKHSTGIDIGDSLT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KQKIVQAGDKDLDGQLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QMIREGGARSLWRGNGINVLKIAPESAIKFMAYEQIKRLVGSDQETLRIHERLVAGSLAG
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                                                                                                                                                                                                                                                                                                                                         Eaton, Dan L.
                                                                                                                                                                                                   Watanabe, Colin Wood, William I.
                                                                                                                                                                                                                                     Gurney, Austin L.
                                                                                                                                                                                                                                                   Grimaldi, Christopher
                                                                                                                                                                                                                                                                      Godowski, Paul J.
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65.8%;
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                                                                                                File
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                                                                                                                                                                                   POLYPEPTIDES
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US-10-063-510-58
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                                                                                                                                                                                                    ; ORGANISM: Homo Sapien US-10-063-510-58
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                                                                                                                       Query Match
Best Local S
Matches 275
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Best Local S
Matches 275
                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/063,510
CURRENT FILING DATE: 2007-05-01
Prior Application removed - See File Wrap:
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 58, Application US/10063510 GENERAL INFORMATION:
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APPLICANT:
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APPLICANT: WOOG, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
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APPLICANT: Filvaroff, E
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TYPE: PRT
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                 LTISEQQAELILQSIDVDGTMTVDWNEWRDYFLFNPVTDIEEIIRFWKHSTGIDIGDSLT 179
                                                           KQKIVQAGDKDLDGQLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLG
                                                                            EEKIFTTGDVNKDGKLDFEEFMKYLKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLG 119
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VKISEQQAEKILKSMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLT
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Godowski, Paul J.
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tive 71; Mismatches
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CURRENT APPLICATION NUMBER: US/10/063,512
CURRENT FILING DATE: 2002-05-01
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 170
SEQ ID NO 58
LENGTH: 469
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TYPE: PRT
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AIAQSSIYPMEVLKTRMALRKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAG
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Grimaldi, Christopher
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SEQ ID NO 58
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ORGANISM: Homo Sapien
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APPLICANT: Filvaroff, El
APPLICANT: Gritsen, Mada
APPLICANT: Goddard, Audr
APPLICANT: Goddwski, Pau
Sequence 58, Application US/10063514
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
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Grimaldi,Christopher
Gurney,Austin L.
Watanabe,Colin K.
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; Prior Application removed - St; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 58
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-514-58
                                                                                                                                                                                                                                                                                                         ; Sequence 58, Application US/10063515
; GENERAL INFORMATION:
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3230R1C1 CURRENT APPLICATION NUMBER: US/10/063,515 CURRENT FILING DATE: 2002-05-01
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                                                                                                        Grimaldi,Christopher J
Gurney,Austin L.
Watanabe,Colin K.
Wood,William I.
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Goddard, Audrey
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Pred. No. 1.5e-114;
71; Mismatches 72;
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GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
                                                                                                          Prior Application removed NUMBER OF SEQ ID NOS: 170 SEQ ID NO 58
            Query Match
Best Local Similarity
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   Matches 275;
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APPLICANT:
APPLICANT:
                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/063,516 CURRENT FILING DATE: 2002-05-01
                                                                                                                                                                   APPLICANT: WOOD, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
                                                                                   LENGTH: 469
TYPE: PRT
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60.5%; Score 1501; DB 6; 65.8%; Pred. No. 1.5e-114; tive 71; Mismatches 72;
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                                                     VKISEQQAEKILKSMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLT
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Search completed: August 18, Job time: 474 sec 2002, 09:28:54

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| 017063 Arabi | 331 Homo sap | 010503 Homo s | 011539 | 708 Huma | 659 Hu | • | Arab | Arab | Arabid | Human | an | Oryz | Arab | | | | | | Dro | Rattus r | | | i Sequence | Caenoi | Arabid | Rattus n | 5 Homo s | Human DN | | Sequence | Homo | Homo sap | Sequence | Homo sap | 7483 | 092326 Seque | C022114 Mus | C019978 Mus | 022637 Mus mus | 56110 Homo : | 90036 Human DN | 13627 Homo | 04161 Oryctola | 23303 Ното вар |

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ALIGNMENTS

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JOURNAL REFERENCE AUTHORS TITLE REFERENCE AUTHORS TITLE KEYWORDS SOURCE ORGANISM DEFINITION. ACCESSION VERSION RESULT AF123303 FEATURES LOCUS JOURNAL source 3259
Homo sapiens calcium-binding
AF123303
AF123303.1 GI:6841065 2 (bases 1 to 3259)
Biery, B. and Valle, D.
Direct Submission
Submitted (25-JAN-1999) Pediatrics/Genetics, Johns Hopkins
University, 725 N. Wolfe Street PCTB 803, Baltimore, MD 213
1. 3259 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom: Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3259)
Biery, B. and Valle, D.
Cloning and subcellular localization of a human calcium-binding Unpublished Homo sapiens transporter human bp mRNA linear PRI 01-FEB-2000
transporter mRNA, partial cds. Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. MD 21205, USA

Result No.

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                                                                      gatgtcaacaaagatgggaagctggattttgaagaatttatgaagtaccttaaagaccat
        CATTCTACAGGAATTGACATAGGGGATAGCTTAACTATTCCAGATGAATTCACGGAAGAC
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                                                                                                                                   ctcaggaacctgggcatccctctgggccaggacgccgaggagaaaatttttactactgga
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AFYKGYVPNLKGIPFAGIDLAVYELLKSYWLDNFAKDSVNPGVMVLLGCGALSSTCG
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2 (bases
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                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
1 (bases 1 to 3298)
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Eukaryota; Metazoa; C
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AF004161
                                            Submitted (14-MAY-1997) Klinik fuer Universitaetsspital, Raemistr. 100,
                                                             Direct Submission
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                                                                                                                                                                                 rabbit
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ctttcgacagatggtaaaaggaggtatccgctcgctttggaggggaaatggtacaaa
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Query Match
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Matches 1771; Conserv
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SSTCGQLASYPLALVETENQAQANLEGAPQLNMVGLFRRIISKEGLPGLYRGITPNEM
KVLPAVGISYVOYENNKQTLGYTQK"
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QGKIEASEIVQSSLQTLGLTISEQQAELILQSIDADGTE
EIIRFWKHSTGIDIGDSLTIPDETEEERKSGOWWRQLLAGGIBAGAVSRTSTAALDLE
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EF-hand motifs
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                                                gaatccgaaatctgaaaatgtactggcttgaacaaaatttgttttgtgtgttagagttat
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E 2 (bases 1 to 170026)

S Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Barran,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., FitzHugh,M., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,G., Kann,L., Karatas,A., Klein,J.,
Howland,J.C., Johnson,R., Jones,G., Kann,L., Karatas,A., Klein,J.,
McEwan,P., McGuran,K., McLaughlin,J., Marquis,N.,
McEwan,P., McGuran,C.H., O'Connor,T., O'Donnell,P.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
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                                                                                                                                                                                                                   Submitted (13-NOV-1999) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 28, 2000 this sequence version replaced gi:6513989
                                                                                                                                    http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                            All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996–1997)
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Unpublished
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Birren, B., Linton, L.,
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Homo sapiens
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Center
Center
                                                          Contact: sequence_submissions@genome
                                                                              Web site: http://www-seq.wi.mit.edu
                                                                                               Center code: WIBR
                                                                                                                      Center: Whitehead Institute/ MIT
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clone RP11-11L4,
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                                 tgactttttctcctcgaattgaaacaagtctatggcaaaagaagctgcatttttttctcaca 1684
TGACTTTTTCTCCTCGAATTGAAACAAGTCTATGGCAAAAGAAGCTGCATTTTTTTCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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119119 119218: gap of control of 50808 l
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Insert size: 169726; sum-of-contigs
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30578 30677: gap of 100 bp
30678 70700: contig of 40023 bp in
70701 70800: gap of 100 bp
70801 119118: contig of 48318 bp in
119119 119218: gap of 100 bp
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119219. .170026
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70801. .119118
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/clone="RP11-11L4"
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98.7%;
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Pred. No. 8.1e-203;
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AL390036.
Homo sapiens
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Mammalia; Eutheria;
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 Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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bm clone RP11-356N1
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Matches 1167; Conser
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                                                                                            tgctgtaggcatcagttatgtggtttatgaaaatatgaagcaaactttaggagtaaccca 1564
                                                                                                                                                                                         CAAAGAAGGAATACCAGGACTTTACAGAGGCATCACCCCAAACTTCATGAAGGTGCTCCC
                                                                                                                                                                                                                  caaagaaggaataccaggactttacagaggcatcaccccaaacttcatgaaggtgctccc 1504
gaaatgatgttgcattttttgctttagcctgataattgaaactttcaacaatctctggag 1624
                                                               TGCTGTAGGCATCAGTTATGTGGTTTATGAAAATATGAAGCAAACTTTAGGAGTAACCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1
RP11-356N1 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers give in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; WP:, WORMPEP; Information on the WORMPEP
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On Sep 7, 2001 this sequence version replaced gi:14456226.
During sequence assembly data is compared from overlapping clones
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
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Submitted (06-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, Submitted (UK. E-mail enquiries: humquery@sanger.ac.uk Clone CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VECTOR: pBACe3.6
This sequence is the entire insert of clone RPI1-356N1 The true roof of clone RPI1-483I13 is at 170175 in this sequence. The roof of clone RPI1-483I13 is at 170175 in this sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           end of clone RP11-483I13 is at 17 right end of clone RP11-320L5 is
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Sequence from overlapping clone RP11-320L5 (AL391235). Assembly confirmed by restriction dige 174215. .175019 /note="Cpg island" /evidence=not_experimental 38180 c 35765 g 53273 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="RP11-356N1"
/clone_lib="RPCI-11.2"
48723. .49036
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(AL391235). Assembly confirmed by restriction dig
79012. . . 79019
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1. .183037
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/db_xref="taxon:9606"
/chromosome="1"
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98.6%;
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Pred. No. 1.6e-202;
0; Mismatches 14;
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RESULT AL356110

DEFINITION LOCUS

Homo sapiens chromosome SEQUENCING IN PROGRESS

IN PROGRESS ***,

159384 bp DNA linear HTG 15-MAY-2000 ne 1 clone RP4-562N20 map p34.1-34.2, *** ; ***, 71 unordered pieces.

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         gaacttgctgtttgcaatatgggcagccacaaagggggagaga
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; LO8752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 112062 bases at least Q40
Consensus quality: 126393 bases at least Q30
Consensus quality: 139133 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coverage: 2.22x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert size: 152384; sum-of-contigs
Insert size: 119983; 3.4% error; agard
Quality coverage: 1.75x in Q20 bases;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: humquery@sanger.ac.uk
----- Proiect Informa
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On Jul 15, 2000 this sequence version replaced gi:7899229.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (14-MAY-2000)
CB10 1SA, UK. E-mail eng
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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source
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Best Local Similarity 90.5%;
Matches 1160; Conservative
                                     59270
                                                                                                       59210
                                                                                                                                                                          1346 ctacccattggctttggtgagaactcgcatgcaggctcaagccatgttagaaggttcccc 1405
                                                     1466 ttacagaggcatcaccccaaacttcatgaaggtgctccctgctgtaggcatcagttatgt 1525
                                                                                                                                                                                                                                                                            1286 tggagtcatggtgttgctgggatgccgttatccagcacctgtggtcagctggccag 1345
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1526 ggtttatgaaaatatgaagcaaactttaggagtaacccagaaatgatgttgcatttttttg 1585
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                                                                                                                       TTACAAAGGCATCACCCCAAACTTCATGAAGGTGCTCCCTGCTGTAGGCATCAGTTATGT
                                                                                                       ACAGCTGAATATGGTTGGCCTCTTTCGACGTATTATTTCCAAAGAAGGAATACCAGGACT
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141739 141838: gap of 10
141839 144713: contig of 28
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139114 13913: gap of
139114 140439: contig of
40440 14055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157144 157243: gap of 100 bp
157244 158253: contig of 1010 bp in length
158254 158353: gap of 100 bp
158254 159384: contig of 1031 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_fragment:00354
fragment_chain:1"
3502. .5184
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fragment_chain:1"
5285. .8399
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1 118745: contig of 1
6 118845: gap of 1
16 121003: contig of 2
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/db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="RP4-562N20"
/clone_lib="RPCI-4"
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136276: gap of
137352: contig of
137452: gap of
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132322: contig of
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136176: cont
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Pred. No. 1.6e-200;
0; Mismatches 120;
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of 2651 bp in 1
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RESULT

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Qy

| | 2546 ggcaqccacaaagggggagaga 2567 60348 GGCAGCACAAAGGTGAGAGATA 60369 | Db Qy |
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| 2545 60347 | 2486 tgatgggctttatttctccctcactggtgaatatcctttgaacttgctgtttgcaatatg | Оy |
| 2485 60289 | 2426 cattettagtaacetgaaatttettttttaattgeatgaagtggattgateatgageaag | Qу |
| 2425 60229 | 2366 gtcctttgtttcctaccttttgaatcagattccgttttagtcaggaagacttcttgggac | Qy Db |
| 2365 60169 | 2306 agcaggaaacgaaattttttgacttgtatcagcttctgcagagcatctttgttttccttt | Qy Db |
| 2305 | 2246 taccaacacaaggcaatttatttgaaagattccgtttatcctgccattgctttgaaaagc | Оy |
| 2245 60049 | 2186 actgtaccattatttggttcctggagttatacactaattttcagtatattactgttaaat | Qy Db |
| 2185 59989 | 2126 aatttetgaagggaagtgatgaaattatatttattteagtgggeaettttecattttace | Qy Db |
| 2125 59929 | 2066 aagtatagggtttatgtccttatttttctttcagctgaatacgaatgaacacagtggtgg | Qy Db |
| 2065 59869 | 2006 agaaccattaatagaaaatcattacatttaaaatataccttacagcaaaagcatccaaat | Фр |
| 2005 59809 | 1946 tttaaatttottgttttatatattttgaatgtotttatagatttotttaaatttoottat | Dp QA |
| 1945 59749 | 1886 agagttataaatcattaatctttatttcgggttggtttacgtttatgccagttcctttata | Оу |
| 1885 59689 | 1826 totgocotgaatoogaaatotgaaaatgtaotggottgaacaaaatttgttttgt | DЬ |
| 1825 59629 | 1766 aatgtgttttgaaaaggccacacaattatactttatctttctt | Qy Db |
| 1765 59569 | 1706 gtcacttcaaacttttgggctaaattatatgtacacaggaaatgttcaaaatcatagtttt | Qy Db |
| 1705 59509 | 1646 aaacaagtctatggcaaaaggaagctgcatttttttcacaaaagggaagacggtaacaatg | Оу |
| 1645 59449 | 1586 ctttagcctgataattgaaactttcaacaatctctggagtgactttttctcctcgaattg | Фр |
| 59389 | | Db |

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BC022637
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DEFINITION
ACCESSION
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Best Local S
Matches 851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                  993
                                                                                  933
                                                   61
ataggaacatttgagagatttatttctggttccatggctggagcaactgcacagactttt
                                                                                                                                    ggtatccgctcgctttggaggggaaatggtacaaacgtcatcaaaatttgctcctgagaca
                                                                   GGAATCCGTTCCCTTTGGAGAGGAAATGGCACCAATGTCATCAAAATAGCTCCCGAGACA
                                                 851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
Web site:
    http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mod@paxil.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can through the I.M.A.G.E. Consortium/LLML at: http://image.llr Series: IRAK Plate: 43 Row: h Column: 13 This clone was selected for full length sequencing because passed the following selection criteria: Hexamer frequency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (01-FEB-2002) National Institutes of Health, Mammaliar Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dickson, M., Schmutz, J., Grinwood, J., Rodriquez, R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg, R.
Direct Submission
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BC022637
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                                                                                                                                                                                                                                                                                   293
                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:4208509"
/tissue_type="Colon, normal. 5
/clone_lib="NCI_CGAP_CO24"
/lab_host="DH10B"
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/protein_id="AAH22637.1"
/protein_id="AAH22637.1"
/db_xref="Gi:18490466"
/translation="GIRSLWRGNGTNVIKIAPETAVKFWAYEQYKKLLTEEGQKLGTF
ERFISGSMAGATAQTFTYPMEYLKTRLAVAKTGQYSGTYGCAKKLLKHEGEFGAFYKGY
IPNLIGIIFYAGIDLAVYELLKSYWLDNFAKDSVNFGVMVLLSCGALSSTCGQLASYP
LALVRTMAQAQATVEGAPQLSWYGLFQRIVSKEGVSGLYRGITPNFMKYLPAVGISYV
VYENNKQTLGVAQK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector:
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Rodentia;
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IMAGE:4208509,
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Pred. No. 4.6e
0; Mismatches
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ismatches 203;
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DEFINITION LOCUS

Mus musculus, IMAGE: 4239441,

Similar to mRNA,

2555 bp ar to KIAA1896 p , complete cds.

protein,

clone MGC:28954

22-JAN-2002

BC019978

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house mouse musculus

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Direct Submission
Submitted (19-DEC-2001) National Institutes of Health, Mammalian Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer General National 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              through the I.M.A.G.E. Consortium/LLNL at: http:/
Series: IRAK Plate: 37 Row: m Column: 7
This clone was selected for full length sequencing passed the following selection criteria: Hexamer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/cdna/contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Huly
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (DNA Sequencing by: Baylor College of Medicine Human Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Richards, S., Gibbs, R.A.
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nilarity 64.9%;
Conservative
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YEOMKRLVGSDOETLRIHERLVAGSLAGAIAQSSIYPMEVLKTRMALRKTGQYSGMLD
CARRILAKEGVAAFYKGYIPNMLGIIPYAGIDLAVYETLKNTWLQRYAVNSADFGVFV
LLACGTISSTCQQLASY PLALVRTWQQQASIEGAPEVTMSSLFKQILRTEGAFGLYR
GLAPNFMKVIPAVSISYVVYENLKITLGVQSR*
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/organism="Mus musculus"
/db_xref="taxon:10000"
/clone="MGC:28954 IMAGE:4239441"
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Location/Qualifiers
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/db_xref="GI:18043565"
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/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B"
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                                                  aggagaaaatttttactactggagatgtcaacaaagatgggaagctggattttgaagaat
                           AGCAGAAAATTGTGCAAGCAGGTGACAAGGACCTTGATGGGCAACTGGACTTTGAAGAGT
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BC022114.1
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Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Genome Sequence Centre,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Parbhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (24-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone was selected for full length sequencing because passed the following selection criteria: Hexamer frequency analysis, GenomeScan gene prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       through the I.M.A.G.E. Consortium/LLNL at Series: IRAK Plate: 57 Row: e Column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            George Yang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="MGC:3638 IMAGE:5098924"
/tissue_type="Liver, normal. 5 mon
/clone_lib="Norl-CGAP_Li9"
/lab_host="DH10B"
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                                                                                                                                                                                                                                           LLACGTISSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKQILRTEGAFGLYR
GLAPNFMKVIPAVSISYVVYENLKITLGVQSR"
a 675 c 710 g 567 t
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PLDRLKVLMQVHASRSNIMCIVGGFTQNIREGCAKENGROGINVLKIAPESAIKFMA
YEQMKRLVGSDQETLRIHERLVAGSLAGAIAQSSIYRWLKFTBMALRKTGQYSGMLD
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 4.7e-92;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C
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Eukaryota; Metazoa; Chordata; Craniai Mammalia; Eutheria; Primates; Catarri 1 (bases 1 to 3712)
Nagase,T., Kikuno,R. and Ohara,O. Prediction of the coding sequences of XXI. The complete sequences of 60 new code for large proteins DNA research: an international journ reports on genes and genomes. 8 (4),
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                      aaaaatccggacaatggtggaggcattttggcaggaggcattgctggtgctgtctctc
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AQSSIYPMEVLKTRMALKTGQYSGMLDCARRILAREGYAAFYKGYVPNNLGIIPYAG
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SIEGAPEVTMSSLFKHILRTEGAFGLYRGLAPNEMKVIPAVSISYVVYENLKITLGVQ
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HYLQDHEKKLRLVFKSLDKKNDGRIDAQEIMGSLDDFWKISEQQAEKILKRIRTGHF
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VEERQTGMWWRHLVAGGGAGAVSRTCTAPLDRLKVLMQVHASRSNNMGIVGGFTQMIR
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<206. .1912
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/db_xref="taxon:9606"
/clone="fk06388"
/tissue_type="brain"
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                                                                              AK054901.1 GI:16549528 oligo capping; fis (full insert sequence). Homo sapiens cerebellum cDNA to mRNA, clonectone:BRACE2007401.
                                                                                                                                                                                    AK054901 2857 bp mRNA linear PRI 31-OCT-2 Homo sapiens cDNA FLJ30339 fis, clone BRACE2007401, moderately similar to Oryctolagus cuniculus peroxisomal Ca-dependent solute
                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                     Homo sapiens
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                  (sites)
Yamazaki, M.,
                                Chordata;
Primates;
Watanabe, K.,
                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                           AAGAATGGCGCGACCACTTCCTGTTGCATTCGCTGGAAAATGTGGAGGACGTGCTGTATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951), Fax:81-438-52-3952)

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center. National Institute of Technology and
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                             AAGCAGCTGGTGGCCGCGCAGTGGCAGGTGCCGTGTCACGGACAGGCACGGCCCCTCTG
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NPDPGAQQGISSEGDADPDGGLDEERSRYLQBERGRLLMFHSLDRNCDGHIDVSEI
QOSFRALIGISISLEDARRISTLHSMDDGTMTIDWQEWRDHFLHSLENVEDDLYFWRHS
TVLDIGECLTVPDEFSKQEKLIHSMDROTMTIDWQEWRDHFLHSLENVEDDLYFWHAS
TVLDIGECLTVPDEFSKQEKLIHSMDROTMTIDWJENSKAYSGITAPLDRLKVFMQVHAS
KTNRLMIFGGLRSMVLEGGIRSIMFGNGINVLKIAPESAIKFWAYBQIKRAILGQQET
LHVDBRFLAGSLAGATAQTIIYFMFULKTRLTLRRTTGQYKGLLDCARRILLEREGTRAL
YRGYLPNMLGIIPYACTDLAVYEMLQCFWYKSGRDMGDPSGLVSLSVTLSTTCGQMA
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591 c
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/db_xref="GI:18128717"
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/db_xref="taxon:9606"
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                                                                                                                                                 1 (bases 1 to 1294)
Wiemann, S., Weil, B., Wellenreuther, R., Gassenhuber, J., Glassl Ansorge, W., Boecher, M., Bloecker, H., Bauersachs, S., Blum, H., Lauber, J., Duesterhoeft, A., Beyer, A., Koehrer, K., Strack, N., Mewes, H.W., Ottenwaelder, B., Obermaier, B., Tampe, J., Heubner, Wambutt, R., Korn, B., Klein, M. and Poustka, A.

Toward a Catalog of Human Genes and Proteins: Sequencing and Analysis of 500 Novel Complete Protein Coding Human cDNAs Genome Res. 11 (3), 422-435 (2001)
Martinsried, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Ca
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
                                                        Ansorge, W., Wirkner, U., Mewes
Direct Submission
Submitted (15-MAY-1999) MIPS,
                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
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                                                                                               Mewes, H.W.,
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                                                          Am Klopferspitz 18a,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of German Genome Project.

This clone (DKFZp586G0123) is available at the RZPD in Berlin Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 140 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at the clone and the sequencing project is available.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.mips.biochem.mpg.de/proj/cDNA/.
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25. .3
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25. .315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical protein"
/protein_id="CAB62534.1"
/db_xref="GI:6562166"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="uterus"
/clone_lib="586 (synonym: hute1). Vector pSport1;
DH10B; sites NotI + Sall/MluI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp586G0123"
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Pred. No. 1.9e-65;
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Mismatches
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                                                                                                                  gacaatggtggaggcagcttttggcaggaggcattgctggtgctgtctctctgaacaagca 771
                                                                                                                                                                                 TTGATGTGGGTGAGAATCTAACGGTCCCGGATGAGTTCACAGTGGAGGAGAGGCAGACGG
CGGCCCCCTGGACAGGCTCAAGGTGCTCATGCAGGTCCATGCCTCCCGCAGCAACAACA
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LL
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie
Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Direct Submission
Submitted (26-MAR-2001) National Institutes of Health, Mammalian Submitted (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Trastitute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be for through the I.M.A.G.B. Consortium/LLNL at: http://lmage.llnl.gov series: IRAL Plate: 11 Row: e Column: 21
This clone was selected for full length sequencing because it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2757 bp
Homo sapiens, clone IMAGE:3530123,
EC005163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 passed the following selection criteria:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR"
1 710 c 843 g 605 t
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/protein_id="AAH55163.1"
/protein_id="AAH55163.1"
/db_xref=="Gi:13477373"
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FMAYEDIKKLYGSDDEFTLRIHBRLVAGSLAGALAQSSIYPMEVLKTRWALKIRPESAIK
FMAYEDIKKLYGSDDEFTLRIHBRLVAGSLAGALAQSSIYPMEVLKTRWALKIRPESAIK
MLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNSADPG
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/clone_lib="NIH_MGC_17"
/lab_host="DH10B-R"
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/db_xref="taxon:9606"
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Pred. No. 4.6e-62;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Sequence 471 from
AX340224
                    cancer
Patent: WO 0196388-A 471 20-DEC-2001;
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Jiang,Y.,
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Primates;
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/db_xref="taxon:9606"
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96.0%;
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Search completed: August 18, 2002, 08:23:49 Job time: 19296 sec

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Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antitheumatic; antiarthritic; antiasthmatic; antiantinflammatory; antithyroid; antiallergic; antibacterial; cardi
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dermatological; neuroprotective; thrombolytic; coagulant; vasotropic; antipsoriatic; antianglogenic; gene therapy; i immune disorder; haematopoietic cell disorder; autoimmune allergic reaction; graft versus host disease; organ reject haemostatic; thrombolytic; cardiovascular disorder; infect neurological disease; drug screening; ss.
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Claim
                                   useful
                                                     Novel
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)B; AAB43451.
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                               isolated nucleic for treating or
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                                                   peptides
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AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral; cardiant; thrombolytic; coagulant; noutropic; vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in the exemplification of AAC78457 and AAB44240 represent sequences used in the exemplification of the present invention.

Sequence 1090 BP; 328 A; 175 C; 174 G; 411 T; 2 other;

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                                    tttttcacaaaagggaagatggtaacaatggtcacttcaaacttttgggctaaattata
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                                                                                                      Human
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or ameliorating medical conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland,
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19-MAY-2000
07-JUN-2000
07-JUL-2000
07-JUL
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Best Local Similarity 64.2
Matches 826; Conservative
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse; skin cell; cytostatic; antiinflammatory; anti-HIV; nootropic; neuroprotective; vulnerary; immunomodulatory; vaccine; keratinocyte growth stimulation; cancer; angiogenesis inhibition; inflammation; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
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Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast; embryonic skin cell; keratinocyte stem cell; transit amplifying c secreted; transmembrane; inflammation; cancer; neurological disea

cDNA encoding

murine ADP/ATP

transporter family protein,

SEQ ij

NO:262

cell;

27-MAR-2000

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AAZ61789

standard;

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                                                                                                                                                                                                                                                                                                                                              CC The invention relates to novel nucleic acid sequences derived from rat CC dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, CC and mouse embryonic skin, keratinocytes stem cells and transit amplifying CC cells. Polypeptides of the invention may be used to treat inflammation, CC cancer and neurological diseases. The proteins may be used to stimulate CC the growth and motility of keratinocytes, to inhibit the growth of CC cancer cells, to modulate angiogenesis and tumour vascularisation, to CC inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, Skin wounds and hair follicle CC disorders. Sequences AAZ61606-Z61832 represent cDNA sequences derived CC conseveral mouse, rat or human skin cell types. Sequences CC AAZ61606-Z61649, AAZ61725-Z61765, AAZ61802-Z61811 and AAZ61826 encode CC proteins with an N-terminal signal sequence, indicating that the proteins care secreted. Sequences AAZ61650-Z61668, AAZ61766-Z61780, AAZ61812-Z61817 CC and AAZ61827-Z61829 encode proteins with one or more putative
                                                                                                                                                                                                                                                                        Matches
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Best Local
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RESULT
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ВP

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Matches 807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
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AAZ65058 standard; CDNA; ВP

AAZ65058

05-APR-2000 (first entry)

Membrane-bound protein PRO1106 encoding

Membrane-bound pharmaceutical; polypeptide; PRO polypeptide;
; receptor immunoadhesin; gene mapping; LDL receptor; TIE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                are useful as hybridization probes, in chromosome and gene mapping the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, espect
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<u>agatggtaaaagaaggaggtatccgctcgctttggaggggaaatggtacaaacgtcatca</u>
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                                  tgctcatgcaggtccatgcctcccgcagcaacaacatgggcatcgttggtggcttcactc
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                                                                                                                                                                       tcccggatgagttcacagtggaggagaggcagacggggatgtggtggagacacctggtgg
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biology, including use as
e and gene mapping. -
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J, Gurney
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; 2000US-0199397.
; 2000WO-US14042.
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Watanabe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 543.8; DB 22
Pred. No. 4.1e-112;
0; Mismatches 437;
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02-JUN-1999;
23-JUN-1999;
07-JUL-1999;
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cell death; cance
diagnostic assay;
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                                                                       2000WO-US08439
99WO-US12252.
99US-0141037.
99US-0143048.
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                                                                                                                                                                                                                                            The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins or an invention describes have cytostatic activity. The PRO proteins or an invention of an invention of a consistency of bloactive molecules, such as compared to take the product of the produce transfer of anti-sense RNA chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF4470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65310 represent human PRO polynucleotide and protein consequences of the present invention.
                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUL-1999
26-JUL-1999
28-JUL-1999
17-AUG-1999
17-SEP-1999
15-SEP-1999
16-OCT-1999
08-OCT-1999
01-DEC-1999
16-DEC-1999
16-DEC-1999
20-DEC-1999
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16-JAN-2000
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015-MAR-2000
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Roy MA,
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Ferrara N,
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                aaaataatgatggaaaaattgaggcttcagaaattgtccagtctctcccagacactgggtc
                                                                     ttatgaagtaccttaaagaccatgagaagaaaattgaaatttggcatttaagagtttagaca
aaaagaatgatggacgcattgacgcgcaggagatcatgcagtccctgcgggacttgggag
                                                                                                              agcagaaaattgtacaagctggagataaggaccttgatgggcagctagactttgaagaat
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                                                                                                                                                                     Similarity 64.8 06; Conservative
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N, Fong S, Gerber H, Gerritsen ME, Goddard
CJ, Gurney AL, Kljavin IJ, Napier MA, Pan
Stewart TA, Tumas D, Watanabe CK, Williams
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2000WO-US00375
2000WO-US00375
2000WO-US03755
2000WO-US04241
2000WO-US04414
2000WO-US04414
2000WO-US05841
2000WO-US058841
2000WO-US05884
2000WO-US0588777
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99US-0146598
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99US-0149396
99WO-US21090
99WO-US21547
99US-0158663
99WO-US28313
99WO-US28310
99WO-US30095
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as toxins, radiolabels or antibodies,
targeted cell death -
                                                                                                                                                                       0;
                                                                                                                                                                     Score 543.8; DB 22;
Pred. No. 4.1e-112;
D; Mismatches 437;
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27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to polynucleotides (AAK51456-AAK5345) and the encoded polypeptides (AAK9323-AAM80302) that exhibit activity elating to encoded polypeptides (AAK98323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating
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ARESULT T AND ALE TO THE TERM Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat; mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia; cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation; nervous system disorder; inflammatory disorder; cell differentiation; ds; angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn; genetic disorder; bone regeneration; tendon; ligament; tissue repair; cytostatic; antirheumatic; antiarthritic; vulnerary; antiinflammatory; antibacterial; immunosuppressive; vasotropic; antiparkinsonian; neuroprotective; osteopathic; antidiabetic; antiasthmatic; anti immunostimulant; analgesic; gene therapy.

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07-SEP-2001

28-FEB-2000; 18-MAY-2000; 17-JUN-2000; 14-JUL-2000; 19-SEP-2000; 26-FEB-2001; ; 2000US-0515126. ; 2000US-0577409. ; 2000US-0597707. ; 2000US-0516807. ; 2000US-0664641. 2001WO-US04926

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cartilage, tendons and ligaments and in tissue repair and burn healing. Note: Some sequences for this patent did not form part of the printed specification, but were obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences AAS44576-AAS44919 represent full-length polynucleotides a contig polynucleotides encoding polypeptides of the invention. The and protein sequences are useful for the treatment, diagnosis and prevention of various types of disorder in a mammalian subject such
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                                                                                                                                                                                                                    attaatgtactcaagattgcccccgagtcagctatcaagttcatggcctatgaacagatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>gagtgcctgacagtgccggacgagttctcaaagcaagagaagctgacgggcatgtggtgg</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cgagctctgggcatttccatctcgctggagcaggctgagaaaattttgcacagcatggac
                                                     aaacatgaaggcttgggagctttttacaaaggctatgttcccaatttattaggtatcata
                                                                              ctgaccttgcgccggacgggccagtataaggggctgctggactgcgccaggcgtatcctg
                                                                                                                                     tccctggctggtgccacagcccaaaccatcatttaccctatggaggtgctgaagacgcgg
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Pred. No. 5.
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5.4e-110;
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                                                                                                                                                                                                                               02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antianaemic; gene therapy; cancer; proliferative disorder; hypertension neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antiferantic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   allergy; aplastic anaen
bone damage; cartilage
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                           P-PSDB;
                                                                                                                                                                                                                                                                                                                31-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      05-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thrombosis; contraceptive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ORFX ORF2093 polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC76538 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200058473-A2
                                                                                                                                                                        (CURA-)
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                                                         2000-602362/57
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                                                                                                                                                                                                                            99US-0127607.
99US-0127636.
99US-0127728.
2000US-0540763.
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                                                                                                               Leach
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   damage; antiinflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO:4185
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neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1562
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Qγ

Query Match Best Local Similarity Matches 738; Conser

Conservative

0;

Mismatches

406;

Indels

0;

Gaps

0

Length 1481;

18.5%;

Score 494.4; DB 21; Pred. No. 3.7e-101;

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immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; cantidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; cantidinflammatory; antibacterial; antiviral; antifungal; antirheumatic; cantidipolical and antianaemic. The sequences can be used for determining contitutions associated with an OREX-associated disorder. The protein and sasociated with an OREX-associated disorder. The concleic acids can be used to express OREX proteins in gene therapy concleic acids can be used to express OREX proteins in gene therapy considerative disorders, neurodegenerative disorders, osteoarthritis, constending the proteins and nucleic acids may be used to treat cancers, considerative disorders, osteoarthritis, consideration, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, consideration, burns, wounds, bone and cartilage damage, concturnal haemoglobinuria, antiinflammatory disease; to enhance consideration; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC74446 to AAC77606 encode the proteins given in AAB40237 to which represent the human ORFX open reading frames 1 to 3161 sequences have activities such as: cytostatic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
Sequence
  1481
BP; 331
A; 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5507pp; English.
ç;
465
G;
273
т;
1 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to AAB43397,
51. The ORFX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vulnerary;
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955
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aacagtacaagaagttacttactgaagaaggacaaaaaaataggaacatttgagagattta
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                                                                                gaaatggtacaaacgtcatcaaaattgctcctgagacagctgttaaattctgggcatatg
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| ttacotccaagatcatgagaaaaaactgaggctgtt tgatggaaaaattgaggcttcagaaattgtccagtctci | ggagaaaatttttactactggagatgtcaacaaagatgggaagctggaf | Query Match 20.4%; Score 545.4; DB 3; Length Best Local Similarity 64.9%; Pred. No. 1.2e-130; Matches 807; Conservative 0; Mismatches 436; Indels | RESULT 1 US-09-188-930-262 ; Sequence 262, Application US/09188930A ; Patent No. 6150502 ; GENERAL INFORMATION: APPLICANT: Watson, James D. APPLICANT: Steeman, Lorna APPLICANT: Sleeman, Matthew APPLICANT: Onrust, Rene APPLICANT: Murison, James Greg TITLE OF INVENTION: Compositions Isolated From Skin Cells TITLE OF INVENTION: and Methods For Their Use FILE REFERENCE: 11000.1011c1 CURRENT APPLICATION NUMBER: US/09/188,930A CURRENT FILING DATE: 1998-11-09 NUMBER OF SEQ ID NOS: 348 SOFTWARE: FastSEQ for Windows Version 3.0 ; SEQ ID NO 262 LENGTH: 1816 TYPE: DNA CRGANISM: Mouse US-09-188-930-262 | ALIGNMENTS | 44 42.4 1.6 1092 2 US-08-646-590B-35 45 42.4 1.6 1092 4 US-09-412-184-35 | 2 43.2 1.6 23673 4 US-09-773-816-1 3 43 1.6 6124 4 US-08-213-419B-3 | 0 43.4 1.6 436/6 3 US-09-356-952-12 1 43.2 1.6 906 1 US-08-100-874-1 | 9 43.6 1.6 8220 2 US-08-487-8268-11 | 3/ 43.6 1.6 8220 2 US-08-232-463-14 | 36 43.6 1.6 1519 1 US-07-971-759-19 | 34 43.8 1.6 4810 3 US-08-852-629-11 | 3 43.8 1.6 1511 2 US-08-544-332-8 | 32 43.8 1.6 1511 1 IIS-08-107-7554-8 | 30 43.8 1.6 660 2 US-08-544-332-32 | 29 43.8 1.6 660 1 US-08-107-755A-32 | 28 43.8 1.6 660 1 US-07-991-867B-32 |
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Sequence 23, Application US/09188930A
Patent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Orust, Rene
APPLICANT: Murison, James Greg
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SOFTWARE: FASTSEQ
SEQ ID NO 23
LENGTH: 997
TYPE: DNA
ORGANISM: mouse
US-09-188-930-23
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Best Local Similarity
Matches 504; Conserv
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Pred. No. 3.1e
0; Mismatches
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3.1e-77;
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; OTHER INFORMATION: score 5.6
; OTHER INFORMATION: seq WHFLASFFPRAGC/HG
US-08-905-223-87
RESULT 4
US-08-232-463-14/c
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Best Local Similarity
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ORIGINAL SOURCE:
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LENGTH: 437 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEPAX: (619) 235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: WOTO SOFTWARE: WOTO DATA:
CURRENT APPLICATION DATA:
US/08/905,223
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compati
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TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
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                                                                                                                                                                                                   280
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                                                                400 AGAATGATGGACGCATTGACGCGCAGGAGATCATGCAG 437
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TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE
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                                                                                                                                                    tgaagtaccttaaagaccatgagaagaaaatgaaattggcatttaagagtttagacaaaa 438
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ISTaelsen, Ned A.
ISTAELSEN, 29,655
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. 8.7e-13;
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                               IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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NAME: BENT, Stephen A.
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                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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493 gtctgactatttctgaacaacaagcagagttgattcttcaaagcattgatgttgatggga 552
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CTTY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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OPERATING SYSTEM:
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                                                                                                                  aatttatgaagtaccttaaagaccatgagaagaaaatgaaattggcatttaagagtttag 432
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22313-0299
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WENTION: RECOMBINANT FOWLPOX VIRUS
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(703)683-4109
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                            DB 1;
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US-08-487-826B-13
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Best Local :
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                                                                                                                                                                                                    Matches 236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (619) 235-017
INFORMATION FOR SEQ ID NO:
                                                                                                                                  17469 GATATATATGTGGATCATAATAATGTGACTAATAATAATATGGATGTACCTACTAAAATG 17528
 17589
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APPLICANT:
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APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERVTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
                   1844 tctgaaaatgtactggcttgaacaaaatttgtttttgtgtgtttagagttataaatcattaa 1903
                                                                                                  1784
                                                                                                                                                              1724 gctaaattatatgtacacagaaatgttcaaaatcatagttttaatgtgttttgaaaaggc 1783
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LENGTH: 19124 base pai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
HYPOTHETICAL:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Knobbe Martens Olson & Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Israelsen, Nec
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                              cacacaattatactttatctttcttaataatcctgcaaatctctgccctgaatccgaaa 1843
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Chitnis, Chetan
Miller, Louis H.
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Pred. No. 0.0025;
0; Mismatches 285; Indels
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US-09-014-969-14/c
; Sequence 14, Application US/09014969
; Patent No. 5965397...
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US-09-014-969-14
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APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward
                                                                                                                      TELEFAX: (617) 876-58 INFORMATION FOR SEQ ID NO:
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                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
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                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Sprunger, Suzanne
                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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                MOLECULE TYPE:
                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                             NAME: Sprunger, Suzanne A. REGISTRATION NUMBER: 41,323
                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 02140
                                   TOPOLOGY:
                                                  STRANDEDNESS:
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                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cambridge
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87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Merberg, David
Treacy, Maurice
Spaulding, Vikki
Agostino, Michael J.
TVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
EVENTION: ENCODING THEM
SEQUENCES: 32
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US-07-867-106-2
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                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5852 base pairs
TYPE: NUCLEIC ACID
TYPE: Single
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Best Local S
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                                                                                                               TOPULCE: IYPE: I
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                               FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                   NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RIG
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02 NOV-1989
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Improved Plasmid Vectors for Cellular TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1991 tttaaatttccttatagaaccattaatagaaaatcattacatttaaaatataccttacag 2050
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                                                                                                    FEATURE:
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                                                                                                                                               STRANDEDNESS: si
TOPOLOGY: linear
                                                                 LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                 NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                     TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
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STREET: One Liberty Place 46th Floor
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Chang, Andy C M
Williams, Keith L
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Best Local S
Matches 105
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 33
LENGTH: 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 33, Application US/09247373B Patent No. 6168954
                                                                                                                                                                                                                                                                                                                       LOCATION: (1101)
OTHER INFORMATION: NAME/KEY: unsure
LOCATION: (1104)
OTHER INFORMATION: NAME/KEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: CL-1108-A
CURRENT APPLICATION NUMBER: US/09/247,373B
CURRENT FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 08/924,747
PRIOR FILING DATE: 1997-09-05
NUMBER OF SEQ ID NOS: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEPE, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                  NAME/KEY: unsure LOCATION: (1116) OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: SOYBEAN
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: unsure
                                                                                             1051
                                                                                                                                              1871 tttgtttttgtgtgttagagttataaatcattaatctttatttcgggtggtttacgtttat 1930
2051 caaaagcatccaaataa
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                                                                 tttaaatttccttatagaaccattaatagaaaatcattacatttaaaatataccttacag
                                                                                                           gccagttcctttatattttaaatttcttgtttttatatttttgaatgtctttatagatttc 1990
                                        ATTGAATTATGATTTATTGCCATCAATATAAATATATTATTAGTTAAGCTACATAAGAG
                                                                                            104;
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Pred. No. 0.0019;
2; Mismatches 91;
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US-07-867-106-4
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Patent No. 5389526
GENERAL INFORMATION:
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Best Local Similarity 50.4%;
                                                                                                                                                                                                                                                                                                                Matches
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INFORMATION FOR SEQ ID NO:
                                                                                                      1985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. STREET: One Liberty Place 46th Floor
                                    2045
                                                                      2026
                                                                                                                                                                                           1906 tttatttcgggttggtttacgtttatgccagttcctttatattttaaatttcttgttttata 1965
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                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 3138 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
DEFERENCE COCCEPT NUMBER: 51,14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
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APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith
 2086 tatt 2089
                                                                                                                                        1966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: NUCLEIC ACID STRANDEDNESS: single
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                                                       attacatttaaaatataccttacagcaaaagcatccaaataagtatagggtttatgtcct 2085
                                  tattttgaatgtotttatagatttotttaaattttoottatagaaccattaatagaaaatc 2025
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Improved Plasmid Vectors for Cellular
Slime Moulds of the Genus Dictyostelium
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                                                                                                                                                                                                                                                                                            Best Local Similarity 51.3
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                           15657
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                    2051 caaaagcatccaaataagtatagggtttatgtccttatttttcttt 2096
                                                                                                                                                                         1931 gccagttcctttatatttaaatttcttgttttatatatttttgaatgtctttatagatttc 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/487,826B FILING DATE: 10-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING D
TITLE OF INVENTION: AND PLASM
NUMBER OF SEQUENCES: 45
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APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David
                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Israelsen, Ned
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STRANDEDNESS: sing
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                                                                                    INFORMATION
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ID NO: 13:
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AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
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Pred. No. 0.015;
0; Mismatches 11
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US-08-485-284A-1
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                                                                                                                                                                                                                                                Matches
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                                                                                                                                                      1921
                   1861 ttgaacaaaatttgtttttgtgtgtttagagttataaatcattaatctttatttcgggtggt 1920
                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP 43361/1992
FILING DATE: 28-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/025,416
FILING DATE: 01-MAR-1993
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
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                                                                                                                      757 TTACTCTTTTGGGAATTAAATAATAATTATATCATATACCCATATCACATTTTACTATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
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                                                                                                                                                                                  TTTAATAAAATAGCCTGTTTCTGTTTCTGTTTTATATTATACAATTTTTTATCCTAATAA 756
TCTTTTCCATCATCATCATCATCATCACGAGTTTTCGGTTATCAATACTCTTTTCAT 936
                                                           tatagatttctttaaatttccttatagaaccattaatagaaaatcattacatttaaaata 2040
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20005-3918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (202) 822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HATANAKA, HARUYO
IVENTION: NOVEL VECTOR HAVING PROMOTER THAT IS
IVENTION: INDUCIBLE BY METHANOL AND/OR GLYCEROL
                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                        unknown
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)N: 435
                                                                                                                                                                                                                                                                                                                                        genomic DNA
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                                                                                                                                                                                                                                                             Score 49.8; DB Pred. No. 0.004;
                                                                                                                                                                                                                                             Mismatches 157; Indels 0;
                                                                                                                                                                                                                                                                        DB 1;
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US-08-343-428-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                         TELEFAX: (212)596-9090 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                               NAME: Haley, Jr., James F.
REGISTRATION NUMBER: 27794
REFERENCE/DOCKET NUMBER: SH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 19-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Haley, Jr., James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Fis
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                        MOLECULE TYPE: (
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 18-NOV-: CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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TITLE OF INVENTION: No. 5665586el Protease
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                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JAPAN APPLICATION NUMBER: JAPAN 1992
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                                                                                                                                                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/
FTI.ING DATE: 30-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: New York
                                                                                                                       NAME/KEY:
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                                                                                                                                                                                            ORGANISM:
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                                                                                                                                                                                                                                               STRANDEDNESS:
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                                        NAME/KEY:
                                                                                                                                                     LOCATION:
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                                                    IDENTIFICATION
                                                                 LOCATION:
                                                                                                                                    IDENTIFICATION METHOD:
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           DENTIFICATION
                                                                                             DENTIFICATION
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10020-1104
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Tsuzuki, Hiroshige
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                        METHOD:
peptide
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                                                                                                                      signal
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          METHOD:
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US-08-998-416-1137
; Sequence 1137, Application US/08998416
; Patent No. 6239264
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Best Local :
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                 INFORMATION FOR
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: ĞENOMIC DNA SEQU
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                           TELECOMMUNICATION INFORMATION: 919-541-8587
                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                             FILING DATE: 31-DEC-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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CITY: Research Triangle Park
STATE: No. 6239264th Carolina
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                                                                            NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38, REFERENCE/DOCKET NUMBER:
                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
                                                                                                                                                                                                                                                                  SOFTWARE:
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                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gggccaggacgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
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CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rebischung, Corinne
VENTION: GENOMIC DNA SEQUENCES
                          919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wendland, Jurgen
Knechtle, Philipp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pohlmann, Rainer
Steiner, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mohr, Christine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                   PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                      No. 6239264artis Corporation
                 SEQ ID
                                                                                                                                                                                                     24-DEC-1997
N: 435
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                                                                              PF/5-30306/A/CGC1976
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Pred. No. 0.005;
0; Mismatches 154; Indels
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RESULT 14
US-07-945-283-1
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                                                                                                                                                                                                                  Sequence 1, Application US/07945283
Patent No. 5352596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.8%;
Best Local Similarity 45.2%;
Matches 261; Conservative
                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis P. Ribando
                                                                                                                                       APPLICANT: Cheung, Andrew K.
APPLICANT: Wesley, Ronald D.
TITLE OF INVENTION: Pseudora
TITLE OF INVENTION: Involvin
COMPUTER READABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1878
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ORIGINAL SOURCE:
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                                                                                                                           NUMBER OF SEQUENCES:
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                                                            STREET:
CITY: F
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              COUNTRY: UZIP: 61604
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                                               STATE:
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                                                                                                                                                                                                                                                                                                                                                                                 tgtgtgttagagttataaatcattaatctttatttcgggtggtttacgtttatgccagtt 1937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTATTATTTTATTATATATATCTATTTTATAAATATTATGTTGATTTATATTATTTAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tgcaaatctctgccctgaatccgaaatctgaaatgtactggcttgaacaaaatttgttt 1877
                                                           Peoria
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FORM:
                                                                           5352596th University
                                                                                                                                       Pseudorabies Virus Deletion Mutants Involving The EPO and LLT Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 49.2; DE Pred. No. 0.003 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

US/07/945,283

19920911

OPERATING SYSTEM: F SOFTWARE: PatentIn

compatible
PC-DOS/MS-DOS
In Release #1.0, Version

#1.25

MEDIUM TYPE:

IBM PC

Floppy disk

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US-08-998-416-186

Sequence 186, Application US/08998416

Patent No. 6239264

GENERAL INFORMATION:
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US-07-945-283-1
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Best Local
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                              4493
                                                                                                4673 CGCTCGAGGACGCCGCGGCAGGCCAGGA 4700
                                                                                                                                                4613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 27976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 309-685-4011 ext.513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECCE: NO
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LENGTH: 8438 base pair
   APPLICANT:
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                                                                                                                     292 gcatccctctgggccaggacgccgagga 319
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                            Local Similarity 51.9 les 108; Conservative
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                                                                                                                                              Ribando, Curtis P
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Philippsen, Peter
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Pred. No. 0.03;
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
1818
                                                                                                                                                                                                                                                               1758 atagttttaatgtgttttgaaaaggccacacaattatactttatcttttcttaataatcc 1817
                                                                                                                                                                                                                                                                                                                 1698 taacaatggtcacttcaaacttttgggctaaattatatgtacacagaaatgttcaaaatc 1757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: CH 0 FILING DATE: 31-DEC-1996 ATTORNEY/AGENT INFORMATION: NAME: Meigs, J. Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                         1878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: GENOMIC DNA SEQUITITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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ZIP: 27709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                cctttatattttaaatttcttgttttatatattttgaatgtctttatagatttctttaaat 1997
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EDNESS: single
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Knechtle, Philipp
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Steiner, Sabine
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Search completed: August 18, 2002, 08:14:03 Job time: 17844 sec

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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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BI962667
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17743.953 Million cell updates/sec
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BM450214 AGENCOURT
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AK015371 Mus muscu
BE731210 601567293
BF729622 60187136
BI158686 602921763
BI962667 1e53b05.y
AL599428 DKFZp313M
BF132795 60154594
BE885075 601510825
BB623288 BB623288
BG894729 355456 MA
BF884680 355388 MA
BF18710 602075750
BF570740 602075750
                                                                                                                                                                                Description
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KEYWORDS
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | ω 5 | 34 | ω ω | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 |
| 294.6 | 298.8 | 299 | 300.6 | 303.4 | 305.2 | 321.2 | 326.2 | 328.8 | 332.8 | 337 | 340 | 340 | 347.2 | 351.2 | 365 | 365.2 | 369.2 | 369.8 | 371.2 | 380.2 | 388.8 | 389.4 | 390.2 | | 424.4 | 430.4 | 439.4 |
| • | • | 11.2 | | | | | | | | | | | • | | | | | | | | | | | 15.8 | 15.9 | | 16.4 |
| 824 | 859 | 560 | 940 | 543 | 889 | 750 | 477 | 477 | 437 | 944 | 519 | 365 | 518 | 1022 | 501 | 735 | 853 | 480 | 784 | 386 | 682 | 720 | 685 | 720 | 898 | 858 | 506 |
| 10 | 9 | 10 | 9 | 10 | 10 | 10 | 9 | 9 | 9 | 10 | 9 | 10 | 10 | 9 | 9 | 10 | 10 | 9 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 9 |
| вG209392 | AL564670 | BJ040514 | AL555116 | BG360178 | BF691873 | BG623074 | вв858108 | BB857423 | BE127029 | BI828204 | BB855418 | W52586 | BG473584 | AL555731 | BB853428 | BG778203 | BG538950 | AA024208 | BE569071 | W39750 | вм491099 | ВJ072734 | BG779437 | BG773095 | BF572032 | BF697486 | AA001086 |
| BG209392 RST28907 | , | 4 | AL555116 AL555116 | | BF691873 602248457 | 4 | вв858108 вв858108 | | BE127029 DEPA0778 | • | BB855418 BB855418 | W52586 zc91h01.rl | BG473584 602515929 | | | BG778203 602666363 | 0 | 3 | BE569071 601339373 | W39750 zc80a08.r1 | BM491099 pgp2n.pk0 | | | | 60207787 | 6 6021293 | AA001086 ze47c08.r |

ALIGNMENTS

RESULT 1 BM450214 LOCUS DEFINITION BASE COUNT REFERENCE ACCESSION AUTHORS TITLE ORGANISM JOURNAL source 1020 bp mRNA linear E AGENCOURT_6393362 NIH_MGC_72 Homo sapiens cDNA clone 5', mRNA sequence. BM450214 Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC/DCTD/DTP NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) found through the I.M.A.G.E. Consortium/LLNL at: http://image.11pl.gov Platte: LLAM12204 row: o column: 10 High quality sequence stop: 619. Location/Qualifiers Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 1020) Homo sapiens EST BM450214.1 GI:18499254 human. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can 315 ۵ /clone_lib="NIH_MGC_72" /tissue_type="melanotic melanoma" /lab host="DH10B (phage-resistant)" /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI; /site_2: SalI; Cloned unidirectionally. Primer: Oligo of the period of the primer of the pr /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5528289" .1020 269 g Craniata; Ve Catarrhini; 253 Library constructed by Life Vertebrata; i; Hominidae; Euteleostomi; Homo. EST 05-FEB-2002 e IMAGE:5528289 be

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http://image.llnl.gov
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National Institutes of Health, Mammalian
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/db_xref="taxon:9606"
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El (bases 1 to 1117)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (Morpholished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Aaron Hsueh

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies of Clone distribution wGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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Location/Qualifiers
    /organism="Mus musculus"
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/note="Organ: ovary, PMSG-treated; Vector:
pCMV-SPORT6.ccdb; Site_1: EcoRV; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.2 kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."
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Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokoham Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
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1674 bp mRNA linear HTC 19-JAN-2002

Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4930443612:homolog to PEROXISOMAL CA-DEPENDENT
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                                                                                                                                                               Direct Submission
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mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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303, 19-44 (1999)
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GGAACTCCTTGTTTAGCGAAGACACGGAGAAGGAGATTTTTATGGATGCAGATTCCAATG
                                                                                    TGGACCACAATGGAGATGGTGTGGTGGACATCACGGAGCTCAGGGATGGGCTGAAACACT
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Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Division of Experimental Animal Research in Riken contributed to
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DIVRFWKHSTILDIGESISLDEFTEDEKMSGEMWRRLVAAGIASATTRTCTPAPLERL
KVTMQVOSLKVNKMGLYHMFKQMVKEGGFFSGEKMSGEWWRRLVAAGIASATIRTCTPAPLERL
KVTMQVOSLKVNKMGLYHMFKQMVKEGGFFSGTVYPMLKTRLNLSKTGEVSGLVDCVRKY
KLLSPDGDHLGVLQFTAGCMAGATSQTCVPDMEVIKTRLNLSKTGEVSGLVDCVRKY
LLKREGIQAFSKGYVPNLLSIIPYAGLLDTIFELLKNHWLEHYAGNSVNPGIAIVLGCS
TVSHTCGQLASEPLLLVRTRMQAVMLEKETVRMMQLIQEIYTKEGKKGFFRGFTPNVL
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/db_xref="MGD:MGI:1907887"
/db_xref="taxon:10090"
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                                                    GTAGCACAGTGTCACACACTTGTGGCCAGTTAGCCAGTTTTCCACTGATTCTTGTTAGAA
                                                                                                       ACTGGCTAGAACACTATGCAGGAAACTCGGTGAATCCTGGAATAGCAATTGTGCTGGGTT
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National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 980)
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                                                                                                                                                                                                                                                                                                               /tissue_type="choriocarcinoma"
//lab_host="DHIOB (phage-resistant)"
//lab_host="DHIOB (phage-resistant)"
//note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
//note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGAGG(). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Callifornia, Berkeley) using ZAP-CDNA synthesis Xit (Stratagene) and Superscript II RT (Life Technologies)."
a 232 c 275 g 211 t
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/db_xref="taxon:9606"
/clone="IMAGE:3842039"
/clone_lib="NIH_MGC_21"
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Pred. No. 2.3e-91;
0; Mismatches 30;
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Mammalia; Eutheria; Primates; Catar
1 (bases 1 to 839)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mamm
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/clone_lib="NIAGE.54"
/tissue_type="from chronic myelogenous leukemia"
/tissue_type="from chronic myelogenous leukemia"
/lab_host="DHIDB (T1 phage-resistant)"
/lab_host="DHIDB (T1 phage-resistant)"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site_l: Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc);
Site_l: Sfil (ggccgctcggc); Site_3: (ggccattatggcc);
Site_l: Sfil (ggccgccycgcc); Site_2: Sfil (ggccattatggcc);
Site_1: Sfil (ggccgccycgcc); Site_2: Sfil (ggccattatggcc);
Site_2: Sfil (ggccgccattatggccc); Site_2: Sfil (ggccattatggcc);
Site_1: Sfil (ggccgccattatggccc); Site_2: Sfil (ggccattatggcc);
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               cggaagacgaaaaaaatccggacaatggtggaggcagcttttggcaggaggcattgctg
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CAGAAGATGAGAAAAAATCAGGACAGTGGTGGAGGCAGCTCCTGGCAGGAGGTGTGGCGG
                                                        TCTGGAAACACTCTACTGGAATTGACATAGGGGATAGTTTAACTATTCCAGATGAATTCA
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BI158686
BI158686.1 GI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia D
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11167 row: n column: 16
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High quality sequence stop: 734.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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602921763F1 NIH_CGAP_Mam3
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="IMAGE:5062095"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="tumor, gross tissue"
/lab_host="DH10B"
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                                                                                                                 Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity A
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                                                                                                                                                                                                                                                                                 Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
                                                                                                      MA 02138
                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 556)
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, Jackson,Y. and Bowers,Y.
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tgtatgagctcttgaagtcctattggctgga-taattttgcaaaagattctgtaaaccc 1285
                                                                                                                              caaaggctatgttcccaattta-ttaggtatcataccttatgcaggcatagatcttgctg 1227
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TGTACGAGCTTTTGAAGTCTTATCGGCTGGATTAACTTTGCCAAAGACTCGGTCAAACC
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556
1e53b05.yl Melton Normalized cDNA 5' similar to TR:Q9UG66
;, mRNA server B1962667.1 ;, mRNA sequence. GI:16337072 bp mRNA linear EST 23-OCT-2001 Human Islet 4 N4-HIS 1 Homo sapiens Q9UG66 HYPOTHETICAL 11.3 KD PROTEIN.

Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.

Unpublished (2000)
Other_ESTs: ie53b05.x1 Endocrine Pancreas Consortium Contact: Douglas Melton, Klaus H. Endocrine Pancreas Consortium Kaestner, & Hiroshi

Tsagareishvili, R., Williams, T

Tel: 617-495-1812 Fax: 617-495-8557

Library was constructed by Dr. Douglas Melton DNA sequencing by Washington University Genome Sequencing Center For information obtaining a clone please contact: Juliana Brown Email: dmelton@biohp.harvard.edu by: 9

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Site_2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

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/sex="Both"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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gggacggagtggtggacatcggcgagctgcaggaggggctcaggaacctgggcatccctc
                   atgttgatgggacaatgacagtggactggaatgaatggagagactacttcttatttaatc
                                                                                                     tccagacactgggtctgactatttctgaacaacaagcagagttgattcttcaaagcattg
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                                                                                 TCCAGACACTGGGTCTGACTATTTCTGAACAAGCAGGAGTTGATTCTTCAAAGCATTG
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                                                                                                                                                                                                                                                   TGGATTTTGAAGAATTTATGAAGTACCTTAAAGACCATGAGAAGAAAATGAAATCGGCAT
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No sl sequence available.

This clone (DKFZp313M1729) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email S. Wiemann@dkfz- heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd. Braunschweig/Germany) within the cDNA sequencing consortium of th
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Contact: Bloecker
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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1 (bases 1 to 505)
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/clone_lib="313 (synonym: hlcc2)"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pTriplEx2; Site_1: SfcDNA-collection"
82 c 135 g 122 t
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/db_xref="taxon:9606"
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Pred. No. 8.2e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plate: LLCM974 row: o column: High quality sequence stop: 534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                     /tissuc_type="muccepidermoid carcinoma"
/tissuc_type="muccepidermoid carcinoma"
/lab_host="bH10B (T1 phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggcgcttgggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-ACKGCCCATMATGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGTGAGCCGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb): 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
                                                                                                                                                                                 Library.
a 148
                                                                                                                                                                                                            Laboratories (Palo Alto, CA). Note: this is
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_59"
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Pred. No. 3.4e-73;
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                                                                                                                       found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
http://image.llnl.gov
Plate: LLAM9730 row: b column: 08
High quality sequence stop: 534.
                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                       National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates;
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3912103"
/clone_lib="NIH_MGC_71"
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 632)
1 (bases 1 to 632)
1 Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
1 Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasak,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Taqami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
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RIKEN full-length enriched, 12
musculus cDNA clone 6720455K09
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/lab_host="DHIOB (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. "
a 254 c 239 g 187 t 1 others
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96.5%;
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Query Match Best Local (Matches

514;

Conservative

0,

Mismatches

l Similarity

17.6%; 87.9%;

Score 471.4; Pred. No. 1.9

.9e-69 DB 9;

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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Ai, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa Ishii, Y. and Hayashizaki, Y. Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Func. Genomics 2 pre, L72-L86 (2001 Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequencing pipeline with 384 multicapillary set 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Y. and Hayashizaki, Y., Y. and Hayashizaki, Y.
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RIKEN Mouse ESTS (Arakawa,T., e
Unpublished (2011)
Contact: Yoshihide Hayashizaki
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e mouse tissues
                          179
                          a
                                                                                                           was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI" 149 c 169 g 135 t
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Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory
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/dev_stage="12 days embryo"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="RIKEN full-length enriched,
male wolffian duct"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Site_1: SalI; Site_2: BamHI; cDNA library
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/strain="C57BL/6J"
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RESULT 1
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and -minmatch 12 options.

PCR PRIMER'S
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 119 row: K column: 13
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                  agacattgaggaaattatccgtttctggaaacattctacaggaattgacataggggatag
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PO Box 166, Clay Co
Tel: 402 762 4366
Fax: 402 762 4390
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355456 MARC
BG894729
BG894729.1
EST.
                                                         Email: smith@email.marc.usda.gov
Single pass sequencing. Bases ca.
v0.980904.e. Vector identified b.
and -minmatch 12 options.
                                                                                                                           EST discovery in swine unpublished (2000)
Contact: Smith TPL USDA, ARS, US Meat Animal Research Center USDA, Clay Center, NE 68933-0166, U
                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 531)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., and Keele,J.W.
                                                                                                                                                                                       Design and use of two
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                                 Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 529)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L.,
Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegre
and Keele, J.W.
                                                                                                          pig.
        Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
Unpublished
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1 92 c 140 g 139 t
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/lab_host="DH10B"
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/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
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Pred. No. 6.8e-68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGAAATGGTACAAATGTCATTAAAATTGCGCCTGAGACAGCTGTTAAGTTCTGGGCATA
                                                                                                                                                                                                                                  ATTTAATCCCGTTACAGACATTGAGGAAATTATCCGTTTCTGGAAACATTCTACCGGTAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGCATTGATGCTGATGGGACAATGACAGTGGACTGGAATGAGTGGAGGGACTACTTCTT 60
                                                                         tgaacagtacaagaagttacttactgaagaaggacaaaaaataggaacatttgagagatt 1012
                                                                                                                                                                                     gggaaatggtacaaacgtcatcaaaattgctcctgagacagctgttaaattctgggcata 952
                                                                                                                                                                                                                        GAACATATATGGTGGCTTTCGACAGATGGTGAAAGAAGGAGGGATCCGCTCCCTTTGGAG
                                                                                                                          TGAACAGTACAAGAAATTGCTTACTGAGGAAGGACAAAAAGTAGGAACTTTTTGAGAGATT
                                                                                                                                                                                                                                                                                                                       ACAGTGGTGGAGGCAGCTCTTGGCAGGAGGTGTTGCCGGCGCCGTCTCTCGAACAAGCAC
                                                                                                                                                                                                                                                                                                                                                                     TGACATAGGAGACAGTTTAACTATTCCGGATGAGTTCACGGAAGATGAAAAAAAGTCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COntact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, US
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and a
v0.989044.e. Vector identified by cross_marks.
BF168710 7
601775935F1 NCI_CGAP_Lu29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BACKWARD: GTTTTCCCAGTCACGACG
Plate: 119 row: O column: 11
Seq primer: ATTTAGGTGACACTATAG.
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PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: Xhc Library made from pooled tissue from day 11, 13, 15, and 30 embryos."

92 c 140 g 138 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.2%;
92.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 460.8; DB 1
Pred. No. 1.2e-67;
0; Mismatches 42
               740 bp
     Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                called and alt_trimmed with phred
d by cross_match with the -minscore
     musculus
               mRNA
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     CDNA
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   linear
A clone
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   EST 30-OCT-2
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AUTHORS
TITLE
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                   Qy
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Matches 597
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                                       502
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les 597; Conserv
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142 tgcgctggctgcgggacttcgcgctgcccaccgcgggcctgccaggacgcggagcagccga 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCGCTGGCTGCGGGCCTT-GTGCTGCCCACCG-GCGCTGCCACGACGCGGAGCCGCC-A 58
                                                                                                                                                                                                           agtaccttaaagaccatgagaagaaaatgaaattggcatttaagagtttagacaaaaata 441
                                                                                                                                                                                                                                                                                                     aaatttttactactggagatgtcaacaaagatgggaagctggattttgaagaatttatga 381
                                                                                                                                                                                                                                                                                                                                                                                            gcgagctgcaggaggggctcaggaacctgggcatccctctgggccaggacgccgaggaga 321
                                                                                                                                                                                        AATACCTGAAAGACCATGAGAAGAAAATGAAATTAGCATTTAAAAAG-TTGGACAAGAATA
                                                                                                                                                                                                                                                                                AAATTTTCACCACTGGCGATGTCAACAAAGATGGGAAGCTGGA-TTTGAAGAATTTATGA
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CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plate: LLAM9266 row: f column:
High quality sequence stop: 668.
Location/Qualifiers
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BF168710
BF168710.1 GI:11049062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 740)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo: Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

a 158 c 216 g 162 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous
Stem cell origin."
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="CZECH II (feral)"
/db_xref="taxon:10090"
/clone="IMAGE:4017416"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 456.4; DB 10;
Pred. No. 6.4e-67;
0; Mismatches 86;
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